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[Continued on next page]

(54) Title: **TRANSPORTERS AND ION CHANNELS**

(57) Abstract: The invention provides human transporters and ion channels (TRICH) and polynucleotides which identify and encode TRICH. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of TRICH.

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TRANSPORTERS AND ION CHANNELS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of transporters and ion channels and to the use of these sequences in the diagnosis, treatment, and prevention of transport, neurological, muscle, immunological, and cell proliferative disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels.

BACKGROUND OF THE INVENTION

Eukaryotic cells are surrounded and subdivided into functionally distinct organelles by hydrophobic lipid bilayer membranes which are highly impermeable to most polar molecules. Cells and organelles require transport proteins to import and export essential nutrients and metal ions including K^+ , NH_4^+ , P_i , SO_4^{2-} , sugars, and vitamins, as well as various metabolic waste products. Transport proteins also play roles in antibiotic resistance, toxin secretion, ion balance, synaptic neurotransmission, kidney function, intestinal absorption, tumor growth, and other diverse cell functions (Griffith, J. and C. Sansom (1998) The Transporter Facts Book, Academic Press, San Diego CA, pp. 3-29). Transport can occur by a passive concentration-dependent mechanism, or can be linked to an energy source such as ATP hydrolysis or an ion gradient. Proteins that function in transport include carrier proteins, which bind to a specific solute and undergo a conformational change that translocates the bound solute across the membrane, and channel proteins, which form hydrophilic pores that allow specific solutes to diffuse through the membrane down an electrochemical solute gradient.

Carrier proteins which transport a single solute from one side of the membrane to the other are called uniporters. In contrast, coupled transporters link the transfer of one solute with simultaneous or sequential transfer of a second solute, either in the same direction (symport) or in the opposite direction (antiport). For example, intestinal and kidney epithelium contains a variety of symporter systems driven by the sodium gradient that exists across the plasma membrane. Sodium moves into the cell down its electrochemical gradient and brings the solute into the cell with it. The sodium gradient that provides the driving force for solute uptake is maintained by the ubiquitous Na^+/K^+ ATPase system. Sodium-coupled transporters include the mammalian glucose transporter (SGLT1), iodide transporter (NIS), and multivitamin transporter (SMVT). All three transporters have twelve putative transmembrane segments, extracellular glycosylation sites, and cytoplasmically-oriented N- and C-termini. NIS plays a crucial role in the evaluation, diagnosis, and treatment of various thyroid pathologies because it is the molecular basis for radioiodide thyroid-imaging

techniques and for specific targeting of radioisotopes to the thyroid gland (Levy, O. et al. (1997) Proc. Natl. Acad. Sci. USA 94:5568-5573). SMVT is expressed in the intestinal mucosa, kidney, and placenta, and is implicated in the transport of the water-soluble vitamins, e.g., biotin and pantothenate (Prasad, P.D. et al. (1998) J. Biol. Chem. 273:7501-7506).

5 One of the largest families of transporters is the major facilitator superfamily (MFS), also called the uniporter-symporter-antiporter family. MFS transporters are single polypeptide carriers that transport small solutes in response to ion gradients. Members of the MFS are found in all classes of living organisms, and include transporters for sugars, oligosaccharides, phosphates, nitrates, nucleosides, monocarboxylates, and drugs. MFS transporters found in eukaryotes all have a structure
10 comprising 12 transmembrane segments (Pao, S.S. et al. (1998) Microbiol. Molec. Biol. Rev. 62:1-34). The largest family of MFS transporters is the sugar transporter family, which includes the seven glucose transporters (GLUT1-GLUT7) found in humans that are required for the transport of glucose and other hexose sugars. These glucose transport proteins have unique tissue distributions and physiological functions. GLUT1 provides many cell types with their basal glucose requirements and
15 transports glucose across epithelial and endothelial barrier tissues; GLUT2 facilitates glucose uptake or efflux from the liver; GLUT3 regulates glucose supply to neurons; GLUT4 is responsible for insulin-regulated glucose disposal; and GLUT5 regulates fructose uptake into skeletal muscle. Defects in glucose transporters are involved in a recently identified neurological syndrome causing infantile seizures and developmental delay, as well as glycogen storage disease, Fanconi-Bickel
20 syndrome, and non-insulin-dependent diabetes mellitus (Mueckler, M. (1994) Eur. J. Biochem. 219:713-725; Longo, N. and L.J. Elsas (1998) Adv. Pediatr. 45:293-313).

Monocarboxylate anion transporters are proton-coupled symporters with a broad substrate specificity that includes L-lactate, pyruvate, and the ketone bodies acetate, acetoacetate, and beta-hydroxybutyrate. At least seven isoforms have been identified to date. The isoforms are
25 predicted to have twelve transmembrane (TM) helical domains with a large intracellular loop between TM6 and TM7, and play a critical role in maintaining intracellular pH by removing the protons that are produced stoichiometrically with lactate during glycolysis. The best characterized H^+ -monocarboxylate transporter is that of the erythrocyte membrane, which transports L-lactate and a wide range of other aliphatic monocarboxylates. Other cells possess H^+ -linked monocarboxylate
30 transporters with differing substrate and inhibitor selectivities. In particular, cardiac muscle and tumor cells have transporters that differ in their K_m values for certain substrates, including stereoselectivity for L- over D-lactate, and in their sensitivity to inhibitors. There are Na^+ -monocarboxylate cotransporters on the luminal surface of intestinal and kidney epithelia, which allow the uptake of lactate, pyruvate, and ketone bodies in these tissues. In addition, there are
35 specific and selective transporters for organic cations and organic anions in organs including the

kidney, intestine and liver. Organic anion transporters are selective for hydrophobic, charged molecules with electron-attracting side groups. Organic cation transporters, such as the ammonium transporter, mediate the secretion of a variety of drugs and endogenous metabolites, and contribute to the maintenance of intercellular pH (Poole, R.C. and A.P. Halestrap (1993) *Am. J. Physiol.* 264:C761-C782; Price, N.T. et al. (1998) *Biochem. J.* 329:321-328; and Martinelle, K. and I. Haggstrom (1993) *J. Biotechnol.* 30:339-350).

ATP-binding cassette (ABC) transporters are members of a superfamily of membrane proteins that transport substances ranging from small molecules such as ions, sugars, amino acids, peptides, and phospholipids, to lipopeptides, large proteins, and complex hydrophobic drugs. ABC transporters consist of four modules: two nucleotide-binding domains (NBD), which hydrolyze ATP to supply the energy required for transport, and two membrane-spanning domains (MSD), each containing six putative transmembrane segments. These four modules may be encoded by a single gene, as is the case for the cystic fibrosis transmembrane regulator (CFTR), or by separate genes. When encoded by separate genes, each gene product contains a single NBD and MSD. These "half-molecules" form homo- and heterodimers, such as Tap1 and Tap2, the endoplasmic reticulum-based major histocompatibility (MHC) peptide transport system. Several genetic diseases are attributed to defects in ABC transporters, such as the following diseases and their corresponding proteins: cystic fibrosis (CFTR, an ion channel), adrenoleukodystrophy (adrenoleukodystrophy protein, ALDP), Zellweger syndrome (peroxisomal membrane protein-70, PMP70), and hyperinsulinemic hypoglycemia (sulfonylurea receptor, SUR). Overexpression of the multidrug resistance (MDR) protein, another ABC transporter, in human cancer cells makes the cells resistant to a variety of cytotoxic drugs used in chemotherapy (Taglicht, D. and S. Michaelis (1998) *Meth. Enzymol.* 292:130-162).

A number of metal ions such as iron, zinc, copper, cobalt, manganese, molybdenum, selenium, nickel, and chromium are important as cofactors for a number of enzymes. For example, copper is involved in hemoglobin synthesis, connective tissue metabolism, and bone development, by acting as a cofactor in oxidoreductases such as superoxide dismutase, ferroxidase (ceruloplasmin), and lysyl oxidase. Copper and other metal ions must be provided in the diet, and are absorbed by transporters in the gastrointestinal tract. Plasma proteins transport the metal ions to the liver and other target organs, where specific transporters move the ions into cells and cellular organelles as needed. Imbalances in metal ion metabolism have been associated with a number of disease states (Danks, D.M. (1986) *J. Med. Genet.* 23:99-106).

Transport of fatty acids across the plasma membrane can occur by diffusion, a high capacity, low affinity process. However, under normal physiological conditions a significant fraction of fatty acid transport appears to occur via a high affinity, low capacity protein-mediated transport process.

Fatty acid transport protein (FATP), an integral membrane protein with four transmembrane segments, is expressed in tissues exhibiting high levels of plasma membrane fatty acid flux, such as muscle, heart, and adipose. Expression of FATP is upregulated in 3T3-L1 cells during adipose conversion, and expression in COS7 fibroblasts elevates uptake of long-chain fatty acids (Hui, T.Y. et al. (1998) J. Biol. Chem. 273:27420-27429).

Mitochondrial carrier proteins are transmembrane-spanning proteins which transport ions and charged metabolites between the cytosol and the mitochondrial matrix. Examples include the ADP, ATP carrier protein; the 2-oxoglutarate/malate carrier; the phosphate carrier protein; the pyruvate carrier; the dicarboxylate carrier which transports malate, succinate, fumarate, and phosphate; the tricarboxylate carrier which transports citrate and malate; and the Grave's disease carrier protein, a protein recognized by IgG in patients with active Grave's disease, an autoimmune disorder resulting in hyperthyroidism. Proteins in this family consist of three tandem repeats of an approximately 100 amino acid domain, each of which contains two transmembrane regions (Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, p. 551; PROSITE PDOC00189 Mitochondrial energy transfer proteins signature; Online Mendelian Inheritance in Man (OMIM) *275000 Graves Disease).

This class of transporters also includes the mitochondrial uncoupling proteins, which create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. The result is energy dissipation in the form of heat. Mitochondrial uncoupling proteins have been implicated as modulators of thermoregulation and metabolic rate, and have been proposed as potential targets for drugs against metabolic diseases such as obesity (Ricquier, D. et al. (1999) J. Int. Med. 245:637-642).

Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form ion-selective pores within the membrane. There are two basic types of ion channels, ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical impulse conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Ion Transporters

Ion transporters generate and maintain the resting electrical potential of a cell. Utilizing the energy derived from ATP hydrolysis, they transport ions against the ion's concentration gradient.

These transmembrane ATPases are divided into three families. The phosphorylated (P) class ion transporters, including $\text{Na}^+\text{-K}^+$ ATPase, $\text{Ca}^{2+}\text{-ATPase}$, and $\text{H}^+\text{-ATPase}$, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of Na^+ and Ca^{2+} are low and cytosolic concentration of K^+ is high. The vacuolar (V) class of ion transporters includes H^+ pumps on intracellular organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of H^+ pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and inorganic phosphate (P_i).

10 The P-ATPases are hexamers of a 100 kD subunit with ten transmembrane domains and several large cytoplasmic regions that may play a role in ion binding (Scarborough, G.A. (1999) *Curr. Opin. Cell Biol.* 11:517-522). The V-ATPases are composed of two functional domains: the V_1 domain, a peripheral complex responsible for ATP hydrolysis; and the V_0 domain, an integral complex responsible for proton translocation across the membrane. The F-ATPases are structurally and evolutionarily related to the V-ATPases. The F-ATPase F_0 domain contains 12 copies of the c subunit, a highly hydrophobic protein composed of two transmembrane domains and containing a single buried carboxyl group in TM2 that is essential for proton transport. The V-ATPase V_0 domain contains three types of homologous c subunits with four or five transmembrane domains and the essential carboxyl group in TM4 or TM3. Both types of complex also contain a single a subunit that
15 may be involved in regulating the pH dependence of activity (Forgac, M. (1999) *J. Biol. Chem.* 274:12951-12954).

The resting potential of the cell is utilized in many processes involving carrier proteins and gated ion channels. Carrier proteins utilize the resting potential to transport molecules into and out of the cell. Amino acid and glucose transport into many cells is linked to sodium ion co-transport
25 (symport) so that the movement of Na^+ down an electrochemical gradient drives transport of the other molecule up a concentration gradient. Similarly, cardiac muscle links transfer of Ca^{2+} out of the cell with transport of Na^+ into the cell (antiport).

Gated Ion Channels

Gated ion channels control ion flow by regulating the opening and closing of pores. The
30 ability to control ion flux through various gating mechanisms allows ion channels to mediate such diverse signaling and homeostatic functions as neuronal and endocrine signaling, muscle contraction, fertilization, and regulation of ion and pH balance. Gated ion channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open their pores in response to mechanical stress; voltage-gated channels (e.g., Na^+ , K^+ , Ca^{2+} , and Cl^- channels) open
35 their pores in response to changes in membrane potential; and ligand-gated channels (e.g.,

acetylcholine-, serotonin-, and glutamate-gated cation channels, and GABA- and glycine-gated chloride channels) open their pores in the presence of a specific ion, nucleotide, or neurotransmitter. The gating properties of a particular ion channel (i.e., its threshold for and duration of opening and closing) are sometimes modulated by association with auxiliary channel proteins and/or post translational modifications, such as phosphorylation.

Mechanically-gated or mechanosensitive ion channels act as transducers for the senses of touch, hearing, and balance, and also play important roles in cell volume regulation, smooth muscle contraction, and cardiac rhythm generation. A stretch-inactivated channel (SIC) was recently cloned from rat kidney. The SIC channel belongs to a group of channels which are activated by pressure or stress on the cell membrane and conduct both Ca^{2+} and Na^{+} (Suzuki, M. et al. (1999) J. Biol. Chem. 274:6330-6335).

The pore-forming subunits of the voltage-gated cation channels form a superfamily of ion channel proteins. The characteristic domain of these channel proteins comprises six transmembrane domains (S1-S6), a pore-forming region (P) located between S5 and S6, and intracellular amino and carboxy termini. In the Na^{+} and Ca^{2+} subfamilies, this domain is repeated four times, while in the K^{+} channel subfamily, each channel is formed from a tetramer of either identical or dissimilar subunits. The P region contains information specifying the ion selectivity for the channel. In the case of K^{+} channels, a GYG tripeptide is involved in this selectivity (Ishii, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656).

Voltage-gated Na^{+} and K^{+} channels are necessary for the function of electrically excitable cells, such as nerve and muscle cells. Action potentials, which lead to neurotransmitter release and muscle contraction, arise from large, transient changes in the permeability of the membrane to Na^{+} and K^{+} ions. Depolarization of the membrane beyond the threshold level opens voltage-gated Na^{+} channels. Sodium ions flow into the cell, further depolarizing the membrane and opening more voltage-gated Na^{+} channels, which propagates the depolarization down the length of the cell. Depolarization also opens voltage-gated potassium channels. Consequently, potassium ions flow outward, which leads to repolarization of the membrane. Voltage-gated channels utilize charged residues in the fourth transmembrane segment (S4) to sense voltage change. The open state lasts only about 1 millisecond, at which time the channel spontaneously converts into an inactive state that cannot be opened irrespective of the membrane potential. Inactivation is mediated by the channel's N-terminus, which acts as a plug that closes the pore. The transition from an inactive to a closed state requires a return to resting potential.

Voltage-gated Na^{+} channels are heterotrimeric complexes composed of a 260 kDa pore-forming α subunit that associates with two smaller auxiliary subunits, $\beta 1$ and $\beta 2$. The $\beta 2$ subunit is a integral membrane glycoprotein that contains an extracellular Ig domain, and its association with α

and $\beta 1$ subunits correlates with increased functional expression of the channel, a change in its gating properties, as well as an increase in whole cell capacitance due to an increase in membrane surface area (Isom, L.L. et al. (1995) Cell 83:433-442).

Non voltage-gated Na^+ channels include the members of the amiloride-sensitive Na^+ channel/degenerin (NaC/DEG) family. Channel subunits of this family are thought to consist of two transmembrane domains flanking a long extracellular loop, with the amino and carboxyl termini located within the cell. The NaC/DEG family includes the epithelial Na^+ channel (ENaC) involved in Na^+ reabsorption in epithelia including the airway, distal colon, cortical collecting duct of the kidney, and exocrine duct glands. Mutations in ENaC result in pseudohypoaldosteronism type 1 and Liddle's syndrome (pseudohyperaldosteronism). The NaC/DEG family also includes the recently characterized H^+ -gated cation channels or acid-sensing ion channels (ASIC). ASIC subunits are expressed in the brain and form heteromultimeric Na^+ -permeable channels. These channels require acid pH fluctuations for activation. ASIC subunits show homology to the degenerins, a family of mechanically-gated channels originally isolated from *C. elegans*. Mutations in the degenerins cause neurodegeneration. ASIC subunits may also have a role in neuronal function, or in pain perception, since tissue acidosis causes pain (Waldmann, R. and M. Lazdunski (1998) Curr. Opin. Neurobiol. 8:418-424; Eglen, R.M. et al. (1999) Trends Pharmacol. Sci. 20:337-342).

K^+ channels are located in all cell types, and may be regulated by voltage, ATP concentration, or second messengers such as Ca^{2+} and cAMP. In non-excitabile tissue, K^+ channels are involved in protein synthesis, control of endocrine secretions, and the maintenance of osmotic equilibrium across membranes. In neurons and other excitable cells, in addition to regulating action potentials and repolarizing membranes, K^+ channels are responsible for setting resting membrane potential. The cytosol contains non-diffusible anions and, to balance this net negative charge, the cell contains a Na^+ - K^+ pump and ion channels that provide the redistribution of Na^+ , K^+ , and Cl^- . The pump actively transports Na^+ out of the cell and K^+ into the cell in a 3:2 ratio. Ion channels in the plasma membrane allow K^+ and Cl^- to flow by passive diffusion. Because of the high negative charge within the cytosol, Cl^- flows out of the cell. The flow of K^+ is balanced by an electromotive force pulling K^+ into the cell, and a K^+ concentration gradient pushing K^+ out of the cell. Thus, the resting membrane potential is primarily regulated by K^+ flow (Salkoff, L. and T. Jegla (1995) Neuron 15:489-492).

Potassium channel subunits of the Shaker-like superfamily all have the characteristic six transmembrane/1 pore domain structure. Four subunits combine as homo- or heterotetramers to form functional K channels. These pore-forming subunits also associate with various cytoplasmic β subunits that alter channel inactivation kinetics. The Shaker-like channel family includes the voltage-gated K^+ channels as well as the delayed rectifier type channels such as the human ether-a-go-go

related gene (HERG) associated with long QT, a cardiac dysrhythmia syndrome (Curran, M.E. (1998) *Curr. Opin. Biotechnol.* 9:565-572; Kaczorowski, G.J. and M.L. Garcia (1999) *Curr. Opin. Chem. Biol.* 3:448-458).

A second superfamily of K⁺ channels is composed of the inward rectifying channels (Kir).
5 Kir channels have the property of preferentially conducting K⁺ currents in the inward direction. These proteins consist of a single potassium selective pore domain and two transmembrane domains, which correspond to the fifth and sixth transmembrane domains of voltage-gated K⁺ channels. Kir subunits also associate as tetramers. The Kir family includes ROMK1, mutations in which lead to Bartter syndrome, a renal tubular disorder. Kir channels are also involved in regulation of cardiac
10 pacemaker activity, seizures and epilepsy, and insulin regulation (Doupnik, C.A. et al. (1995) *Curr. Opin. Neurobiol.* 5:268-277; Curran, *supra*).

The recently recognized TWIK K⁺ channel family includes the mammalian TWIK-1, TREK-1 and TASK proteins. Members of this family possess an overall structure with four transmembrane domains and two P domains. These proteins are probably involved in controlling the resting potential
15 in a large set of cell types (Duprat, F. et al. (1997) *EMBO J* 16:5464-5471).

The voltage-gated Ca²⁺ channels have been classified into several subtypes based upon their electrophysiological and pharmacological characteristics. L-type Ca²⁺ channels are predominantly expressed in heart and skeletal muscle where they play an essential role in excitation-contraction coupling. T-type channels are important for cardiac pacemaker activity, while N-type and P/Q-type
20 channels are involved in the control of neurotransmitter release in the central and peripheral nervous system. The L-type and N-type voltage-gated Ca²⁺ channels have been purified and, though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The α_1 subunit forms the membrane pore and voltage sensor, while the $\alpha_2\delta$ and β subunits modulate the voltage-dependence, gating properties, and the current amplitude of the
25 channel. These subunits are encoded by at least six α_1 , one $\alpha_2\delta$, and four β genes. A fourth subunit, γ , has been identified in skeletal muscle (Walker, D. et al. (1998) *J. Biol. Chem.* 273:2361-2367; McCleskey, E.W. (1994) *Curr. Opin. Neurobiol.* 4:304-312).

The transient receptor family (Trp) of calcium ion channels are thought to mediate capacitative calcium entry (CCE). CCE is the Ca²⁺ influx into cells to resupply Ca²⁺ stores depleted
30 by the action of inositol triphosphate (IP3) and other agents in response to numerous hormones and growth factors. Trp and Trp-like were first cloned from *Drosophila* and have similarity to voltage gated Ca²⁺ channels in the S3 through S6 regions. This suggests that Trp and/or related proteins may form mammalian CCC entry channels (Zhu, X. et al. (1996) *Cell* 85:661-671; Boulay, G. et al. (1997) *J. Biol. Chem.* 272:29672-29680). Melastatin is a gene isolated in both the mouse and human, and
35 whose expression in melanoma cells is inversely correlated with melanoma aggressiveness in vivo.

The human cDNA transcript corresponds to a 1533-amino acid protein having homology to members of the Trp family. It has been proposed that the combined use of malastatin mRNA expression status and tumor thickness might allow for the determination of subgroups of patients at both low and high risk for developing metastatic disease (Duncan, L.M. et al (2001) J. Clin. Oncol. 19:568-576).

5 Chloride channels are necessary in endocrine secretion and in regulation of cytosolic and organelle pH. In secretory epithelial cells, Cl^- enters the cell across a basolateral membrane through an Na^+ , K^+/Cl^- cotransporter, accumulating in the cell above its electrochemical equilibrium concentration. Secretion of Cl^- from the apical surface, in response to hormonal stimulation, leads to flow of Na^+ and water into the secretory lumen. The cystic fibrosis transmembrane conductance
10 regulator (CFTR) is a chloride channel encoded by the gene for cystic fibrosis, a common fatal genetic disorder in humans. CFTR is a member of the ABC transporter family, and is composed of two domains each consisting of six transmembrane domains followed by a nucleotide-binding site. Loss of CFTR function decreases transepithelial water secretion and, as a result, the layers of mucus that coat the respiratory tree, pancreatic ducts, and intestine are dehydrated and difficult to clear. The
15 resulting blockage of these sites leads to pancreatic insufficiency, "meconium ileus", and devastating "chronic obstructive pulmonary disease" (Al-Awqati, Q. et al. (1992) J. Exp. Biol. 172:245-266).

The voltage-gated chloride channels (CLC) are characterized by 10-12 transmembrane domains, as well as two small globular domains known as CBS domains. The CLC subunits probably function as homotetramers. CLC proteins are involved in regulation of cell volume,
20 membrane potential stabilization, signal transduction, and transepithelial transport. Mutations in CLC-1, expressed predominantly in skeletal muscle, are responsible for autosomal recessive generalized myotonia and autosomal dominant myotonia congenita, while mutations in the kidney channel CLC-5 lead to kidney stones (Jentsch, T.J. (1996) Curr. Opin. Neurobiol. 6:303-310).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds
25 to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter binds to their extracellular domain. These channels exist in the postsynaptic membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of Na^+ and produces the initial localized depolarization that activates the
30 voltage-gated channels and starts the action potential. Chloride channels open in response to inhibitory neurotransmitters, such as γ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential. Neurotransmitter-gated ion channels have four transmembrane domains and probably function as pentamers (Jentsch, supra). Amino acids in the second transmembrane domain appear to be important
35 in determining channel permeation and selectivity (Sather, W.A. et al. (1994) Curr. Opin. Neurobiol.

4:313-323).

Ligand-gated channels can be regulated by intracellular second messengers. For example, calcium-activated K^+ channels are gated by internal calcium ions. In nerve cells, an influx of calcium during depolarization opens K^+ channels to modulate the magnitude of the action potential (Ishi et al., *supra*). The large conductance (BK) channel has been purified from brain and its subunit composition determined. The α subunit of the BK channel has seven rather than six transmembrane domains in contrast to voltage-gated K^+ channels. The extra transmembrane domain is located at the subunit N-terminus. A 28-amino-acid stretch in the C-terminal region of the subunit (the "calcium bowl" region) contains many negatively charged residues and is thought to be the region responsible for calcium binding. The β subunit consists of two transmembrane domains connected by a glycosylated extracellular loop, with intracellular N- and C-termini (Kaczorowski, *supra*; Vergara, C. et al. (1998) *Curr. Opin. Neurobiol.* 8:321-329).

Cyclic nucleotide-gated (CNG) channels are gated by cytosolic cyclic nucleotides. The best examples of these are the cAMP-gated Na^+ channels involved in olfaction and the cGMP-gated cation channels involved in vision. Both systems involve ligand-mediated activation of a G-protein coupled receptor which then alters the level of cyclic nucleotide within the cell. CNG channels also represent a major pathway for Ca^{2+} entry into neurons, and play roles in neuronal development and plasticity. CNG channels are tetramers containing at least two types of subunits, an α subunit which can form functional homomeric channels, and a β subunit, which modulates the channel properties. All CNG subunits have six transmembrane domains and a pore forming region between the fifth and sixth transmembrane domains, similar to voltage-gated K^+ channels. A large C-terminal domain contains a cyclic nucleotide binding domain, while the N-terminal domain confers variation among channel subtypes (Zufall, F. et al. (1997) *Curr. Opin. Neurobiol.* 7:404-412).

The activity of other types of ion channel proteins may also be modulated by a variety of intracellular signalling proteins. Many channels have sites for phosphorylation by one or more protein kinases including protein kinase A, protein kinase C, tyrosine kinase, and casein kinase II, all of which regulate ion channel activity in cells. Kir channels are activated by the binding of the $G\beta\gamma$ subunits of heterotrimeric G-proteins (Reimann, F. and F.M. Ashcroft (1999) *Curr. Opin. Cell. Biol.* 11:503-508). Other proteins are involved in the localization of ion channels to specific sites in the cell membrane. Such proteins include the PDZ domain proteins known as MAGUKs (membrane-associated guanylate kinases) which regulate the clustering of ion channels at neuronal synapses (Craven, S.E. and D.S. Brecht (1998) *Cell* 93:495-498).

Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the

transport of molecules across membranes. Defects in the trafficking of membrane-bound transporters and ion channels are associated with several disorders, e.g., cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, von Gierke disease, and certain forms of diabetes mellitus. Single-gene defect diseases resulting in an inability to transport small molecules across membranes include, e.g., cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease (van't Hoff, W.G. (1996) *Exp. Nephrol.* 4:253-262; Talente, G.M. et al. (1994) *Ann. Intern. Med.* 120:218-226; and Chillon, M. et al. (1995) *New Engl. J. Med.* 332:1475-1480).

Human diseases caused by mutations in ion channel genes include disorders of skeletal muscle, cardiac muscle, and the central nervous system. Mutations in the pore-forming subunits of sodium and chloride channels cause myotonia, a muscle disorder in which relaxation after voluntary contraction is delayed. Sodium channel myotonias have been treated with channel blockers. Mutations in muscle sodium and calcium channels cause forms of periodic paralysis, while mutations in the sarcoplasmic calcium release channel, T-tubule calcium channel, and muscle sodium channel cause malignant hyperthermia. Cardiac arrhythmia disorders such as the long QT syndromes and idiopathic ventricular fibrillation are caused by mutations in potassium and sodium channels (Cooper, E.C. and L.Y. Jan (1998) *Proc. Natl. Acad. Sci. USA* 96:4759-4766). All four known human idiopathic epilepsy genes code for ion channel proteins (Berkovic, S.F. and I.E. Scheffer (1999) *Curr. Opin. Neurology* 12:177-182). Other neurological disorders such as ataxias, hemiplegic migraine and hereditary deafness can also result from mutations in ion channel genes (Jen, J. (1999) *Curr. Opin. Neurobiol.* 9:274-280; Cooper, *supra*).

Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia. Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma, and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) *Adv. Pharmacol.* 39:47-98). Various classes of ion channels also play an important role in the perception of pain, and thus are potential targets for new analgesics. These include the vanilloid-gated ion channels, which are activated by the vanilloid capsaicin, as well as by noxious heat. Local anesthetics such as lidocaine and mexiletine which blockade voltage-gated Na⁺ channels have been useful in the treatment of neuropathic pain (Eglen, *supra*).

Ion channels in the immune system have recently been suggested as targets for immunomodulation. T-cell activation depends upon calcium signaling, and a diverse set of T-cell specific ion channels has been characterized that affect this signaling process. Channel blocking agents can inhibit secretion of lymphokines, cell proliferation, and killing of target cells. A peptide antagonist of the T-cell potassium channel Kv1.3 was found to suppress delayed-type hypersensitivity and allogenic responses in pigs, validating the idea of channel blockers as safe and efficacious

immunosuppressants (Cahalan, M.D. and K.G. Chandy (1997) Curr. Opin. Biotechnol. 8:749-756).

The discovery of new transporters and ion channels, and the polynucleotides encoding them, satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of transport, neurological, muscle, immunological, and cell proliferative disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, transporters and ion channels, referred to collectively as "TRICH" and individually as "TRICH-1," "TRICH-2," "TRICH-3," "TRICH-4," "TRICH-5," "TRICH-6," "TRICH-7," "TRICH-8," "TRICH-9," "TRICH-10," "TRICH-11," "TRICH-12," "TRICH-13," "TRICH-14," "TRICH-15," "TRICH-16," "TRICH-17," "TRICH-18," "TRICH-19," "TRICH-20," "TRICH-21," "TRICH-22," "TRICH-23," "TRICH-24," "TRICH-25," "TRICH-26," "TRICH-27," "TRICH-28," "TRICH-29," and "TRICH-30." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-30.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-30. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:31-60.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of

of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group

consisting of SEQ ID NO:31-60, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino

acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target

polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the
5 treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

10 Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for
15 analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

20 Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

25

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing
30 particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a
35 reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so

forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

10 DEFINITIONS

"TRICH" refers to the amino acid sequences of substantially purified TRICH obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of TRICH. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

An "allelic variant" is an alternative form of the gene encoding TRICH. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding TRICH include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as TRICH or a polypeptide with at least one functional characteristic of TRICH. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding TRICH, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding TRICH. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent TRICH. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of TRICH is retained. For example,

negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of TRICH. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind TRICH polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA;

RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense
5 molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

10 The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic TRICH, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

15 "Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide
20 or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding TRICH or fragments of TRICH may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl
25 sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer
30 program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of
35 the protein is conserved and not significantly changed by such substitutions. The table below shows

amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
5	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
10	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
15	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
20	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

5 A "fragment" is a unique portion of TRICH or the polynucleotide encoding TRICH which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 10 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the 15 specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:31-60 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:31-60, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:31-60 is useful, for 20 example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:31-60 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:31-60 and the region of SEQ ID NO:31-60 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-30 is encoded by a fragment of SEQ ID NO:31-60. A fragment 25 of SEQ ID NO:1-30 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-30. For example, a fragment of SEQ ID NO:1-30 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-30. The precise length of a fragment of SEQ ID NO:1-30 and the region of SEQ ID NO:1-30 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended 30 purpose for the fragment.

A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between 35 two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence,

for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment
5 length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

10 The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific
15 hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive
20 conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

25 Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and
30 conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS,
35 for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC

concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of TRICH which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of TRICH which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of TRICH. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of TRICH.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the

antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where
5 necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition.
10 PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an TRICH may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will
15 vary by cell type depending on the enzymatic milieu of TRICH.

"Probe" refers to nucleic acid sequences encoding TRICH, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.
20 "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous
25 nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

30 Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs
35 can be derived from a known sequence, for example, by using computer programs intended for that

purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to
5 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from
10 megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection
15 programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both
20 unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

25 A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have
30 been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a
35 vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is

expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription,
5 translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

10 An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing TRICH,
15 nucleic acids encoding TRICH, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or
20 synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

25 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides
30 by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

35 A "transcript image" refers to the collective pattern of gene expression by a particular cell

type or tissue under given conditions at a given time.

“Transformation” describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term “transformed cells” includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A “transgenic organism,” as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A “variant” of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an “allelic” (as defined above), “splice,” “species,” or “polymorphic” variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to

another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The
 5 presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-
 10 1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

15 THE INVENTION

The invention is based on the discovery of new human transporters and ion channels (TRICH), the polynucleotides encoding TRICH, and the use of these compositions for the diagnosis, treatment, or prevention of transport, neurological, muscle, immunological, and cell proliferative disorders.

20 Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is
 25 denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte
 30 polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

35 Table 3 shows various structural features of the polypeptides of the invention. Columns 1

and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are transporters and ion channels. For example, SEQ ID NO:6 is 89% identical to rat neuronal nicotinic acetylcholine receptor subunit (GenBank ID g6746563) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.7e-188$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:6 also contains a neurotransmitter-gated ion channel domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:6 is a neurotransmitter-gated ion channel. In an alternative example, SEQ ID NO:14 is 93% identical to rat TAP-like ABC transporter (GenBank ID g6045150) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:14 also contains an ABC transporter domain and an ABC transporter transmembrane region as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:14 is an ABC transporter. In an alternative example, SEQ ID NO:16 is 98% identical to human voltage-dependent anion channel (GenBank ID g340199) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.2e-130$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:16 also contains a eukaryotic porin active site domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:16 is a mitochondrial porin. In an alternative example, SEQ ID NO:20 is 28% identical to a rat voltage-gated calcium channel (GenBank ID g4586963) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The

BLAST probability score is $2.4e-27$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. Data from BLIMPS and BLAST analyses provide further corroborative evidence that SEQ ID NO:20 is a voltage-gated calcium channel. In an alternative example, SEQ ID NO:22 is 82% identical to human inhibitory glycine receptor (GenBank ID g31849) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.1e-175$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:22 also contains a neurotransmitter-gated ion channel domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:22 is a neurotransmitter-gated ion channel. In an alternative example, SEQ ID NO:30 is 36% identical to human ATP binding cassette (ABC) -C transporter (GenBank ID g1514530) as determined by the Basic Local Alignment Search Tool (BLAST, see Table 2). The BLAST probability score is $2.3e-127$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:30 also contains ABC transporter domains as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains (see Table 3). Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:30 is an ABC transporter. SEQ ID NO:1-5, SEQ ID NO:7-13, SEQ ID NO:15, SEQ ID NO:17-19, SEQ ID NO:21, and SEQ ID NO:23-29 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-30 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:31-60 or that distinguish between SEQ ID NO:31-60 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 6340750H1 is the identification number of an Incyte cDNA sequence, and BRANDIN01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71911330V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g5110579) which contributed to the assembly of the full length polynucleotide sequences. In addition, the identification numbers in column 5 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation "ENST"). Alternatively, the identification numbers in column 5 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation "NM" or "NT") or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation "NP"). Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. For example, FL_XXXXXX_N₁_N₂YYYYY_N₃_N₄ represents a "stitched" sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYYYY is the number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V). Alternatively, the identification numbers in column 5 may refer to assemblages of exons brought together by an "exon-stretching" algorithm. For example, FL_XXXXXX_gAAAAA_gBBBBB_1_N is the identification number of a "stretched" sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human genomic sequence to which the "exon-stretching" algorithm was applied, gBBBBB being the GenBank identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the "exon-stretching" algorithm, a RefSeq identifier (denoted by "NM," "NP," or "NT") may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
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GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).
5 INCY	Full length transcript and exon prediction from mapping of EST sequences to the genome. Genomic location and EST composition data are combined to predict the exons and resulting transcript.

In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

10 Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

15 The invention also encompasses TRICH variants. A preferred TRICH variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the TRICH amino acid sequence, and which contains at least one functional or structural characteristic of TRICH.

20 The invention also encompasses polynucleotides which encode TRICH. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:31-60, which encodes TRICH. The polynucleotide sequences of SEQ ID NO:31-60, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

25 The invention also encompasses a variant of a polynucleotide sequence encoding TRICH. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding TRICH. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID
30 NO:31-60 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting

of SEQ ID NO:31-60. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of TRICH.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding TRICH, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring TRICH, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode TRICH and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring TRICH under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding TRICH or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding TRICH and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode TRICH and TRICH derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding TRICH or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:31-60 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or

combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler
5 (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers,
10 R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding TRICH may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic
15 DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments
20 adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res.
25 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in
30 length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T)
35 library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence

into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode TRICH may be cloned in recombinant DNA molecules that direct expression of TRICH, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express TRICH.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter TRICH-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of TRICH, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of

homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding TRICH may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser. 7*:215-223; and Horn, T. et al. (1980) *Nucleic Acids Symp. Ser. 7*:225-232.) Alternatively, TRICH itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of TRICH, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active TRICH, the nucleotide sequences encoding TRICH or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding TRICH. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding TRICH. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding TRICH and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression

vectors containing sequences encoding TRICH and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding TRICH. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu, N. (1987) *EMBO J.* 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al. (1993) *Proc. Natl. Acad. Sci. USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding TRICH. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding TRICH can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding TRICH into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of TRICH are needed, e.g. for the production of antibodies, vectors which direct high level expression of TRICH may be used. For example, vectors

containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of TRICH. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such
5 vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; and Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of TRICH. Transcription of sequences
10 encoding TRICH may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.)
15 These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding TRICH may be ligated into
20 an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses TRICH in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-
25 based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.*
30 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of TRICH in cell lines is preferred. For example, sequences encoding TRICH can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector.
35 Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in

enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

5 Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to
10 methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc.
15 Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

20 Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding TRICH is inserted within a marker gene sequence, transformed cells containing sequences encoding TRICH can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding TRICH under the control of a single
25 promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding TRICH and that express TRICH may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR
30 amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of TRICH using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and
35 fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing

monoclonal antibodies reactive to two non-interfering epitopes on TRICH is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and
5 Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding TRICH
10 include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding TRICH, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase
15 such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding TRICH may be cultured under
20 conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode TRICH may be designed to contain signal sequences which direct secretion of TRICH through a prokaryotic or eukaryotic cell membrane.

25 In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity.
30 Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid
35 sequences encoding TRICH may be ligated to a heterologous sequence resulting in translation of a

fusion protein in any of the aforementioned host systems. For example, a chimeric TRICH protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of TRICH activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the TRICH encoding sequence and the heterologous protein sequence, so that TRICH may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled TRICH may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

TRICH of the present invention or fragments thereof may be used to screen for compounds that specifically bind to TRICH. At least one and up to a plurality of test compounds may be screened for specific binding to TRICH. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of TRICH, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which TRICH binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express TRICH, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing TRICH or cell membrane fractions which contain TRICH are then contacted with a test compound and binding, stimulation, or inhibition of activity of either TRICH or the

compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with TRICH, either in solution or affixed to a solid support, and detecting the binding of TRICH to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

TRICH of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of TRICH. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for TRICH activity, wherein TRICH is combined with at least one test compound, and the activity of TRICH in the presence of a test compound is compared with the activity of TRICH in the absence of the test compound. A change in the activity of TRICH in the presence of the test compound is indicative of a compound that modulates the activity of TRICH. Alternatively, a test compound is combined with an *in vitro* or cell-free system comprising TRICH under conditions suitable for TRICH activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of TRICH may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding TRICH or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential

therapeutic or toxic agents.

Polynucleotides encoding TRICH may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding TRICH can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding TRICH is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress TRICH, e.g., by secreting TRICH in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

15 THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of TRICH and transporters and ion channels. In addition, the expression of TRICH is closely associated with brain, liver, tumor, colon, thymus, small intestine, myometrium, testicular, bone marrow neuroblastoma tumor, parotid gland, lung, pituitary gland, and placental tissues, and Pompe's disease. Therefore, TRICH appears to play a role in transport, neurological, muscle, immunological, and cell proliferative disorders. In the treatment of disorders associated with increased TRICH expression or activity, it is desirable to decrease the expression or activity of TRICH. In the treatment of disorders associated with decreased TRICH expression or activity, it is desirable to increase the expression or activity of TRICH.

Therefore, in one embodiment, TRICH or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy,

ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal

5 neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a

10 neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural

15 abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central

20 nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD),

25 akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial

30 myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, ophthalmoplegia, and acid maltase deficiency (AMD, also known

as Pompe's disease); an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED),
5 bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis,
10 polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis,
15 bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid,
20 penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing TRICH or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified TRICH in
25 conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of TRICH may be administered to a subject to treat or prevent a disorder associated with decreased expression or
30 activity of TRICH including, but not limited to, those listed above.

In a further embodiment, an antagonist of TRICH may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRICH. Examples of such disorders include, but are not limited to, those transport, neurological, muscle, immunological, and cell proliferative disorders described above. In one aspect, an antibody which specifically binds

TRICH may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express TRICH.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding TRICH may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRICH including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of TRICH may be produced using methods which are generally known in the art. In particular, purified TRICH may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind TRICH. Antibodies to TRICH may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with TRICH or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to TRICH have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of TRICH amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to TRICH may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma

technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the
5 splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate
antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc.*
Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda,
S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single
10 chain antibodies may be adapted, using methods known in the art, to produce TRICH-specific single
chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be
generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g.,
Burton, D.R. (1991) *Proc. Natl. Acad. Sci. USA* 88:10134-10137.)

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte
population or by screening immunoglobulin libraries or panels of highly specific binding reagents as
15 disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci. USA*
86:3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for TRICH may also be generated.
For example, such fragments include, but are not limited to, $F(ab')_2$ fragments produced by pepsin
digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of
20 the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and
easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D.
et al. (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
specificity. Numerous protocols for competitive binding or immunoradiometric assays using either
25 polyclonal or monoclonal antibodies with established specificities are well known in the art. Such
immunoassays typically involve the measurement of complex formation between TRICH and its
specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies
reactive to two non-interfering TRICH epitopes is generally used, but a competitive binding assay
may also be employed (Pound, *supra*).

30 Various methods such as Scatchard analysis in conjunction with radioimmunoassay
techniques may be used to assess the affinity of antibodies for TRICH. Affinity is expressed as an
association constant, K_a , which is defined as the molar concentration of TRICH-antibody complex
divided by the molar concentrations of free antigen and free antibody under equilibrium conditions.
The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their
35 affinities for multiple TRICH epitopes, represents the average affinity, or avidity, of the antibodies

for TRICH. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular TRICH epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the TRICH-antibody complex must withstand rigorous manipulations. Low-affinity antibody
5 preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of TRICH, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

10 The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of TRICH-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and
15 guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding TRICH, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules
20 (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding TRICH. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding TRICH. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

25 In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995)
30 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et
35 al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.*

25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding TRICH may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in TRICH expression or regulation causes disease, the expression of TRICH from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in TRICH are treated by constructing mammalian expression vectors encoding TRICH and introducing these vectors by mechanical means into TRICH-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of TRICH include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX, PCR2-TOPOTA vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). TRICH may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl.

Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. *supra*), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding TRICH from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to TRICH expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding TRICH under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver

polynucleotides encoding TRICH to cells which have one or more genetic abnormalities with respect to the expression of TRICH. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 389:239-242, both incorporated by reference herein.

10 In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding TRICH to target cells which have one or more genetic abnormalities with respect to the expression of TRICH. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing TRICH to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

25 In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding TRICH to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity

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(e.g., protease and polymerase). Similarly, inserting the coding sequence for TRICH into the alphavirus genome in place of the capsid-coding region results in the production of a large number of TRICH-coding RNAs and the synthesis of high levels of TRICH in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of TRICH into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding TRICH.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques

for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding TRICH. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA
5 constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase
10 linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

15 An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding TRICH. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-
20 macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased TRICH expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding TRICH may be therapeutically useful, and in the treatment of disorders
25 associated with decreased TRICH expression or activity, a compound which specifically promotes expression of the polynucleotide encoding TRICH may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in
30 altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding TRICH is exposed to at least one test compound thus obtained. The sample
35 may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted

biochemical system. Alterations in the expression of a polynucleotide encoding TRICH are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding TRICH. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of TRICH, antibodies to TRICH, and mimetics, agonists, antagonists, or inhibitors of TRICH.

The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising TRICH or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, TRICH or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example TRICH or fragments thereof, antibodies of TRICH, and agonists, antagonists or inhibitors of TRICH, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind TRICH may be used for the diagnosis of disorders characterized by expression of TRICH, or in assays to monitor patients being treated with TRICH or agonists, antagonists, or inhibitors of TRICH. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for TRICH include methods which utilize the antibody and a label to detect TRICH in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring TRICH, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of TRICH expression. Normal or standard values for TRICH expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to TRICH under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of TRICH expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding TRICH may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of TRICH may be correlated

with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of TRICH, and to monitor regulation of TRICH levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding TRICH or closely related molecules may be used to identify nucleic acid sequences which encode TRICH. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding TRICH, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the TRICH encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:31-60 or from genomic sequences including promoters, enhancers, and introns of the TRICH gene.

Means for producing specific hybridization probes for DNAs encoding TRICH include the cloning of polynucleotide sequences encoding TRICH or TRICH derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding TRICH may be used for the diagnosis of disorders associated with expression of TRICH. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease,

cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup

5 disease, and Fanconi disease; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary

10 ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal

15 hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic

20 disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear

25 myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder,

30 ophthalmoplegia, and acid maltase deficiency (AMD, also known as Pompe's disease); an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact

dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding TRICH may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered TRICH expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding TRICH may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding TRICH may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding TRICH in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of TRICH, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding TRICH, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from

normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

5 Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

10 With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development
15 or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding TRICH may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding TRICH, or a fragment of a polynucleotide complementary to the polynucleotide encoding
20 TRICH, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding TRICH may be used to detect single nucleotide polymorphisms (SNPs). SNPs are
25 substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding TRICH are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example,
30 from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis
35 methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the

sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry
5 using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of TRICH include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be
10 accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray
15 can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the
20 activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

25 In another embodiment, TRICH, fragments of TRICH, or antibodies specific for TRICH may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of
30 gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of
35 transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the

hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global

pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by

5 separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by

10 staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the

15 spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

20 A proteomic profile may also be generated using antibodies specific for TRICH to quantify the levels of TRICH expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoze, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed

25 by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor

30 correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such

35 cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding TRICH may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism

(RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding TRICH on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, TRICH, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between TRICH and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with TRICH, or fragments thereof, and washed. Bound TRICH is then detected by methods well known in the art. Purified TRICH can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding TRICH specifically compete with a test compound for binding TRICH. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more

antigenic determinants with TRICH.

In additional embodiments, the nucleotide sequences which encode TRICH may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such
5 properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

10 The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/223,269, U.S. Ser. No. 60/224,456, U.S. Ser. No. 60/226,410, U.S. Ser. No. 60/228,140, U.S. Ser. No. 60/230,067, and U.S. Ser. No. 60/231,434, are hereby expressly incorporated by reference.

15 EXAMPLES

I. Construction of cDNA Libraries

Incye cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incye Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in
20 suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
25 purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

30 In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic
35 oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the

appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,

5 PBLUESCRIPT plasmid (Stratagene), PSPO1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

10 II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid,

15 QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal

20 cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows.

25 Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared

30 using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI

35 protocols and base calling software; or other sequence analysis systems known in the art. Reading

frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing
 5 vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family
 10 databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or
 15 Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention
 20 may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software
 25 Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of
 30 Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the
 35 strength of a match between two sequences (the higher the score or the lower the probability value,

the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:31-60. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization

5 and amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative transporters and ion channels were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode transporters and ion channels, the encoded polypeptides were analyzed by querying against PFAM models for transporters and ion channels. Potential transporters and ion channels were also identified by homology to Incyte cDNA sequences that had been annotated as transporters and ion channels. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

30 "Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information,

generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbprl public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

15 "Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

25 **VI. Chromosomal Mapping of TRICH Encoding Polynucleotides**

The sequences which were used to assemble SEQ ID NO:31-60 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:31-60 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences

had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel (1995) *supra*, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the

entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

5 Alternatively, polynucleotide sequences encoding TRICH are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue;
10 digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following
15 disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding TRICH. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

20 **VIII. Extension of TRICH Encoding Polynucleotides**

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using
25 OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one
30 extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme
35 (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer

pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; 5 Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II 10 (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, 15 digested with CviII cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham 20 Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase 25 (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted 30 with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides 35 designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:31-60 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Skena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection.

After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a

110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μ l of sample mixture consisting of 0.2 μ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source,

although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the TRICH-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring TRICH. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of TRICH. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the TRICH-encoding transcript.

XII. Expression of TRICH

Expression and purification of TRICH is achieved using bacterial or virus-based expression systems. For expression of TRICH in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid

promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express TRICH upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of TRICH in eukaryotic cells is achieved by infecting

5 insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding TRICH by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to

10 infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, TRICH is synthesized as a fusion protein with, e.g., glutathione

15 S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from

20 TRICH at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified TRICH obtained by these methods can be used directly in the assays

25 shown in Examples XVI, XVII, and XVIII, where applicable.

XIII. Functional Assays

TRICH function is assessed by expressing the sequences encoding TRICH at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice

30 include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish

35 transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the

recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of TRICH on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding TRICH and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding TRICH and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIV. Production of TRICH Specific Antibodies

TRICH substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the TRICH amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide and anti-TRICH activity by, for example, binding the peptide or TRICH to a substrate,

blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring TRICH Using Specific Antibodies

Naturally occurring or recombinant TRICH is substantially purified by immunoaffinity chromatography using antibodies specific for TRICH. An immunoaffinity column is constructed by covalently coupling anti-TRICH antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing TRICH are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TRICH (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/TRICH binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and TRICH is collected.

XVI. Identification of Molecules Which Interact with TRICH

Molecules which interact with TRICH may include transporter substrates, agonists or antagonists, modulatory proteins such as G $\beta\gamma$ proteins (Reimann, *supra*) or proteins involved in TRICH localization or clustering such as MAGUKs (Craven, *supra*). TRICH, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled TRICH, washed, and any wells with labeled TRICH complex are assayed. Data obtained using different concentrations of TRICH are used to calculate values for the number, affinity, and association of TRICH with the candidate molecules.

Alternatively, proteins that interact with TRICH are isolated using the yeast 2-hybrid system (Fields, S. and O. Song (1989) *Nature* 340:245-246). TRICH, or fragments thereof, are expressed as fusion proteins with the DNA binding domain of Gal4 or lexA, and potential interacting proteins are expressed as fusion proteins with an activation domain. Interactions between the TRICH fusion protein and the TRICH interacting proteins (fusion proteins with an activation domain) reconstitute a transactivation function that is observed by expression of a reporter gene. Yeast 2-hybrid systems are commercially available, and methods for use of the yeast 2-hybrid system with ion channel proteins are discussed in Niethammer, M. and M. Sheng (1998, *Meth. Enzymol.* 293:104-122).

TRICH may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

Potential TRICH agonists or antagonists may be tested for activation or inhibition of TRICH

ion channel activity using the assays described in section XVIII.

XVII. Demonstration of TRICH Activity

Ion channel activity of TRICH is demonstrated using an electrophysiological assay for ion conductance. TRICH can be expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding TRICH. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A second plasmid which expresses any one of a number of marker genes, such as β -galactosidase, is co-transformed into the cells to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of TRICH and β -galactosidase.

Transformed cells expressing β -galactosidase are stained blue when a suitable colorimetric substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or β -galactosidase sequences alone, are used as controls and tested in parallel. Cells expressing TRICH will have higher anion or cation conductance relative to control cells. The contribution of TRICH to conductance can be confirmed by incubating the cells using antibodies specific for TRICH. The antibodies will bind to the extracellular side of TRICH, thereby blocking the pore in the ion channel, and the associated conductance.

Alternatively, ion channel activity of TRICH is measured as current flow across a TRICH-containing *Xenopus laevis* oocyte membrane using the two-electrode voltage-clamp technique (Ishi et al., *supra*; Jegla, T. and L. Salkoff (1997) J. Neurosci. 17:32-44). TRICH is subcloned into an appropriate *Xenopus* oocyte expression vector, such as pBF, and 0.5-5 ng of mRNA is injected into mature stage IV oocytes. Injected oocytes are incubated at 18 °C for 1-5 days. Inside-out macropatches are excised into an intracellular solution containing 116 mM K-gluconate, 4 mM KCl, and 10 mM Hepes (pH 7.2). The intracellular solution is supplemented with varying concentrations of the TRICH mediator, such as cAMP, cGMP, or Ca^{+2} (in the form of CaCl_2), where appropriate. Electrode resistance is set at 2-5 M Ω and electrodes are filled with the intracellular solution lacking mediator. Experiments are performed at room temperature from a holding potential of 0 mV. Voltage ramps (2.5 s) from -100 to 100 mV are acquired at a sampling frequency of 500 Hz. Current measured is proportional to the activity of TRICH in the assay.

In particular, the activity of TRICH-20 is measured as Ca^{2+} conductance, the activity of TRICH-22 is measured as Cl^- conductance in the presence of glycine, the activity of TRICH-23 is

measured as Ca^{2+} conductance, and the activity of TRICH-24 is measured as K^{+} conductance in the presence of Ca^{2+} , and the activity of TRICH-26 is measured as cation conductance in the presence of heat.

Transport activity of TRICH is assayed by measuring uptake of labeled substrates (including but not limited to, maltose, glucose, or glycogen) into *Xenopus laevis* oocytes. Oocytes at stages V and VI are injected with TRICH mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5mM NaCl, 2.5 mM KCl, 1mM CaCl_2 , 1mM MgCl_2 , 1mM Na_2HPO_4 , 5 mM Hepes, 3.8 mM NaOH, 50µg/ml gentamycin, pH 7.8) to allow expression of TRICH. Oocytes are then transferred to standard uptake medium (100mM NaCl, 2 mM KCl, 1mM CaCl_2 , 1mM MgCl_2 , 10 mM Hepes/Tris-pH 7.5). Uptake of various substrates (e.g., amino acids, sugars, drugs, ions, and neurotransmitters) is initiated by adding labeled substrate (e.g. radiolabeled with ^3H , fluorescently labeled with rhodamine, etc.) to the oocytes. After incubating for 30 minutes, uptake is terminated by washing the oocytes three times in Na^{+} -free medium, measuring the incorporated label, and comparing with controls. TRICH activity is proportional to the level of internalized labeled substrate. In particular, test substrates include sulfate for TRICH-13, tricarboxylates for TRICH-21, dicarboxylates and Na^{+} for TRICH-25, ornithine for TRICH-27, and monocarboxylates for TRICH-28.

ATPase activity associated with TRICH can be measured by hydrolysis of radiolabeled ATP- $[\gamma\text{-}^{32}\text{P}]$, separation of the hydrolysis products by chromatographic methods, and quantitation of the recovered ^{32}P using a scintillation counter. The reaction mixture contains ATP- $[\gamma\text{-}^{32}\text{P}]$ and varying amounts of TRICH in a suitable buffer incubated at 37°C for a suitable period of time. The reaction is terminated by acid precipitation with trichloroacetic acid and then neutralized with base, and an aliquot of the reaction mixture is subjected to membrane or filter paper-based chromatography to separate the reaction products. The amount of ^{32}P liberated is counted in a scintillation counter. The amount of radioactivity recovered is proportional to the ATPase activity of TRICH in the assay.

XVIII. Identification of TRICH Agonists and Antagonists

TRICH is expressed in a eukaryotic cell line such as CHO (Chinese Hamster Ovary) or HEK (Human Embryonic Kidney) 293. Ion channel activity of the transformed cells is measured in the presence and absence of candidate agonists or antagonists. Ion channel activity is assayed using patch clamp methods well known in the art or as described in Example XVII. Alternatively, ion channel activity is assayed using fluorescent techniques that measure ion flux across the cell membrane (Velicelebi, G. et al. (1999) Meth. Enzymol. 294:20-47; West, M.R. and C.R. Molloy (1996) Anal. Biochem. 241:51-58). These assays may be adapted for high-throughput screening using microplates. Changes in internal ion concentration are measured using fluorescent dyes such as the Ca^{2+} indicator Fluo-4 AM, sodium-sensitive dyes such as SBFI and sodium green, or the Cl^{-}

indicator MQAE (all available from Molecular Probes) in combination with the FLIPR fluorimetric plate reading system (Molecular Devices). In a more generic version of this assay, changes in membrane potential caused by ionic flux across the plasma membrane are measured using oxonyl dyes such as DiBAC₄ (Molecular Probes). DiBAC₄ equilibrates between the extracellular solution and cellular sites according to the cellular membrane potential. The dye's fluorescence intensity is 20-fold greater when bound to hydrophobic intracellular sites, allowing detection of DiBAC₄ entry into the cell (Gonzalez, J.E. and P.A. Negulescu (1998) Curr. Opin. Biotechnol. 9:624-631). Candidate agonists or antagonists may be selected from known ion channel agonists or antagonists, peptide libraries, or combinatorial chemical libraries.

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Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

15

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
2194064	1	2194064CD1	31	2194064CB1
2744094	2	2744094CD1	32	2744094CB1
2798241	3	2798241CD1	33	2798241CB1
3105257	4	3105257CD1	34	3105257CB1
3200979	5	3200979CD1	35	3200979CB1
6754139	6	6754139CD1	36	6754139CB1
6996659	7	6996659CD1	37	6996659CB1
7472747	8	7472747CD1	38	7472747CB1
7474121	9	7474121CD1	39	7474121CB1
7475615	10	7475615CD1	40	7475615CB1
7475656	11	7475656CD1	41	7475656CB1
7480632	12	7480632CD1	42	7480632CB1
6952742	13	6952742CD1	43	6952742CB1
7478795	14	7478795CD1	44	7478795CB1
656293	15	656293CD1	45	656293CB1
7473957	16	7473957CD1	46	7473957CB1
7474111	17	7474111CD1	47	7474111CB1
7480826	18	7480826CD1	48	7480826CB1
6025572	19	6025572CD1	49	6025572CB1
5686561	20	5686561CD1	50	5686561CB1
1553725	21	1553725CD1	51	1553725CB1
1695770	22	1695770CD1	52	1695770CB1
4672222	23	4672222CD1	53	4672222CB1
6176128	24	6176128CD1	54	6176128CB1
7473418	25	7473418CD1	55	7473418CB1
7474129	26	7474129CD1	56	7474129CB1
7481414	27	7481414CD1	57	7481414CB1
7481461	28	7481461CD1	58	7481461CB1
7472541	29	7472541CD1	59	7472541CB1
6999183	30	6999183CD1	60	6999183CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	2194064CD1	g2463634	1.60E-41	Monocarboxylate transporter [Homo sapiens] (Price, N. T. et al. (1998) Biochem. J. 329:321-328)
2	2744094CD1	g13346481	0	ATP-binding cassette transporter MRP8 [Homo sapiens]
3	2798241CD1	g1699038	2.90E-142	ABC3 [Homo sapiens] (Connors, T. D. et al. (1997) Genomics 39:231-234)
4	3105257CD1	g8650412	0	M-ABC2 protein [Homo sapiens] (Zhang, F. et al. (2000) Characterization of ABCB9, an ATP binding cassette protein associated with lysosomes J. Biol. Chem. 275:23287-23294)
5	3200979CD1	g1514530	3.10E-119	ABC-C transporter [Homo sapiens] (Klugbauer, N. and F. Hofmann (1996) FEBS Lett. 391:61-65)
6	6754139CD1	g6746563	1.70E-188	neuronal nicotinic acetylcholine receptor subunit [Rattus norvegicus] (Elgoyhen, A. B. et al. (2001) alpha 10: A determinant of nicotinic cholinergic receptor function in mammalian vestibular and cochlear mechanosensory hair cells Proc. Natl. Acad. Sci. U.S.A. 98:3501-3506)
7	6996659CD1	g1050330	0	Ionotropic glutamate receptor [Rattus norvegicus] (Ciabarra, A.M. et al. (1995) J. Neurosci. 15:6498- 6508)
8	7472747CD1	g13926108	1.00E-157	2P domain potassium channel Talk-1 [Homo sapiens] (Girard, C. et al. (2001) Genomic and functional characteristics of novel human pancreatic 2P domain K(+) channels. Biochem Biophys Res Commun. 282:249-256)
9	7474121CD1	g2465542	7.00E-20	TWIK-related acid-sensitive K+ channel [Homo sapiens] (Duprat, F. et al. (1997) EMBO J. 16:5464-5471)
10	7475615CD1	g2654005	5.70E-114	Pendrin [Homo sapiens] (Everett, L.A. et al. (1997) Nature Genet. 17:411-422)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
11	7475656CD1	g3168874	0	Ion channel BCNG-1 [Homo sapiens] (Santoro, B. et al. (1997) Proc. Natl. Acad. Sci. USA 94:14815-14820)
12	7480632CD1	g1514530	9.80E-123	ABC-C transporter [Homo sapiens] (Klugbauer, N. and F. Hofmann (1996) FEBS Lett. 391:61- 65)
13	6952742CD1	g10719650	0	sulfate/anion transporter SAT-1 protein [Homo sapiens] (Lohi, H. et al. (2000) Mapping of Five New Putative Anion Transporter Genes in Human and Characterization of SLC26A6, A Candidate Gene for Pancreatic Anion Exchanger. Genomics 70:102-112)
		g431453	3.10E-276	Sulfate anion transporter [Rattus norvegicus] (Bissig, M. et al. (1994) Functional expression cloning of the canalicular sulfate transport system of rat hepatocytes. J. Biol. Chem. 269:3017-3021)
14	7478795CD1	g6045150	0	TAP-like ABC transporter [Rattus norvegicus] (Yamaguchi, Y. et al. (1999) An ABC transporter homologous to TAP proteins. FEBS Lett. 457:231-236)
15	656293CD1	g6746563	1.30E-220	neuronal nicotinic acetylcholine receptor [Rattus norvegicus]
16	7473957CD1	g340199	1.20E-130	voltage-dependent anion channel [Homo sapiens] (Blachly-Dyson, E. et al. (1993) J. Biol. Chem. 268:1835-1841)
17	7474111CD1	g6006493	1.50E-75	Cardiac potassium channel subunit (Kv6.2) [Homo sapiens] (Zhu, X., et al. (1999) Receptors Channels 6:337-350)
18	7480826CD1	g8248427	1.50E-235	amino acid transporter system A [Rattus norvegicus] (Sugawara, M. et al. (2000) J. Biol. Chem. 275:16473- 16477)
19	6025572CD1	g402628	4.20E-114	adenine nucleotide carrier [Mus musculus]

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
20	5686561CD1	g4586963	2.40E-27	voltage-gated ca channel [Rattus norvegicus] (Ishibashi, K. et al. (2000) Molecular cloning of a novel form (Two-repeat) protein related to voltage-gated sodium and calcium channels. Biochem. Biophys. Res. Commun. 270:370-376)
21	1553725CD1	g545998	1.60E-89	tricarboxylate carrier [Rattus sp.] (Azzi, A. et al. (1993) The mitochondrial tricarboxylate carrier. J. Bioenerg. Biomembr. 25:515-524)
22	1695770CD1	g31849	1.10E-175	inhibitory glycine receptor [Homo sapiens] (Grenningloh, G. et al. (1990) Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization of the corresponding genes. EMBO J. 9:771-776)
23	4672222CD1	g13562153	0	channel-kinase 1 [Homo sapiens] (Ryazanov, A. G. et al. (1999) Alpha-kinases: a new class of protein kinases with a novel catalytic domain Curr. Biol. 9:R43-R45)
24	6176128CD1	g3978472	0	potassium channel subunit [Rattus norvegicus] (Joiner, W.J. et al. (1998) Formation of intermediate-conductance calcium-activated potassium channels by interaction of Slack and Slo subunits. Nat Neurosci. 1:462-469)
25	7473418CD1	g2811122	2.90E-177	NaDC-2 [Xenopus laevis]
26	7474129CD1	g2570933	1.20E-134	vanilloid receptor subtype 1 [Rattus norvegicus] (Caterina, M.J. et al. (1997) The capsaicin receptor: a heat-activated ion channel in the pain pathway. Nature 389:816-824)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
27	7481414CD1	g13445630	1.00E-151	mutant ornithine transporter 2 [Mus musculus] (Wu, Q. and Maniatis, T. (1999) A striking organization of a large family of human neural cadherin-like cell adhesion genes. Cell 97:779-790)
28	7481461CD1	g458247	1.40E-136	X-linked PEST-containing transporter [Homo sapiens] (Lafreniere, R.G. et al. (1994) A novel transmembrane transporter encoded by the XPCT gene in Xq13.2. Mol. Genet. 3:1133-1139)
29	7472541CD1	g6457270	0	Putative E1-E2 ATPase [Mus musculus] (Halleck, M.S. et al. (1999) Differential expression of putative transbilayer amphipath transporters. Physiol. Genomics (Online) 1:139-150)
30	6999183CD1	g1514530	2.30E-127	ABC-C transporter [Homo sapiens] (Klugbauer N. and Hofmann F. (1996) Primary structure of a novel ABC transporter with a chromosomal localization on the band encoding the multidrug resistance- associated protein, FEBS Lett. 391:61-65)

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	2194064CD1	308	S287 S51 T132		Signal peptide: M1-A17 Transmembrane domains: W197-V224, Y248-G270 PEST transporter: DM05037 P53988 1-465:M1-L109, L126-K289 DM05037 Q03064 1-475:M1-L109, V110-K289 DM05037 P36021 155-612:G3-G288	SPScan HMMER BLAST-DOMO
2	2744094CD1	606	S116 S133 S266 S299 S403 S503 S604 S63 T112 T253 T318 T330 T388 T455 T543 T70	N216 N386 N62 N68	Transmembrane domains: P25-W49, Q82-T107, L166-L187, P184-M203 ABC transporter: H392-G575 ABC transporter transmembrane region: S30-A319 ABC transporters family signature: A483-D533 ABC transporter: F502-V516 ATP/GTP binding site: G399-S406 ATP-binding transporter: PD00131:G141-D150, S403-I456, G550-R587 ABC transporters family: DM00008 P33527 1293-1502: F367-G575 DM00008 Q10185 1239-1448: I365-G575 DM00008 P39109 1272-1482: I365-G575 DM00008 S64757 1302-1528: I365-K486 ATP-binding transport protein: PD000130: T61-G292 PD002040: G434-P488	HMMER HMMER-PFAM HMMER-PFAM ProfileScan MOTIFS MOTIFS BLIMPS-PRODOR BLAST-DOMO BLAST-PRODOR

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	2798241CD1	1642	S199 S32 T1366 S431 S443 S1367 S460 S546 T1390 S582 S616 S1405 S624 S761 T1454 S815 S859 T1461 S861 S885 S1558 S962 T28 T1635 T486 T518 T1099 T572 T606 T1126 T779 T780 S1190 T854 Y168 S1236 S1247 S1308 S1372 T1429 Y1552	N190 N388 N458 N499 N576 N86 N943 N973 N996 N1245 N1556 N1627	Transmembrane domains: Q34-M52, S272-P292, S295-F313, V327-I346, I401-L427, V865-H883, P1075-Y1098, L1095-P1114, W1137-I1162, I1165-I1184 ABC transporter: G507-G689, G1326-G1509 ABC transporters family signature: V595D646, I1413-D1464 ABC transporter: L615-V629 ATP/GTP binding sites: G514-S521, G1333-S1340 ABC transporters family: DM00008 P41233 839-1045:I478-S687, K1313-M1506 ABC transporters family: DM00008 P34358 611-816:I478-S687, I1319-M1506 DM00008 P26050 8-212:K1313-S1508, I478-I686 DM00008 P41233 1851-2058:R1309-S1508, I478-I686	HMMER HMMER-PFAM ProfileScan MOTIFS MOTIFS BLAST-DOMO BLAST-DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
4	3105257CD1	659	S206 S26 S300 S452 S504 S583 S62 T261 T284 T293 T348 T520 T615 Y121 Y298	N131 N210	ABC transporter: G441-G628 ABC transporter transmembrane region: L92-I366 ABC transporters family signature: A535-D586 ABC transporter: L555-L569 ATP/GTP binding site: G448-S455 ABC transporters family: BL00211: L446-V457, L555-D586 ATP-binding transporter: PD00131: G190-D199, S452-I505, G603-L640 ABC transporters family: DM00008 A42150 367-576: L413-L625 DM00008 P34712 1076-1290: F415-G628 ATP-binding transport protein: PD000130: L135-Y358 Multidrug resistance ATP-binding transport protein: PD167072: W486-G552	HMMEP-PFAM HMMEP-PFAM ProfileScan MOTIFS MOTIFS BLIMPS-BLOCKS BLIMPS-PRODUM BLAST-DOMO BLAST-PRODUM BLAST-PRODUM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5	3200979CD1	1592	S125 S187 T1117 S207 S386 T1135 S453 Y906 T1214 S714 S733 T1346 S745 S770 T1388 S778 S874 T1417 S882 S994 S1454 T368 T439 T1494 T484 T542 T1580 T565 T673 S1116 T691 T706 S1206 T766 T1257 T782 T801 T1264 T927 T98 T1265 Y1192 S7 S1297 S1320 T77 S1328 T1434 T1466	N185 N62 N75 N870 N871 N899 N949 N1164 N1273	Transmembrane domains: I265-V285, I296-I315, M319-L340, I390-F410, I815-M834, L1063-M1082, W1099-T1117, L1126-L1145 ABC transporter: G500-G642, G1281-G1465 ABC transporters family signature: L1372-D1420 ATP/GTP binding sites: G507-S514, G1288-S1295 ABC transporters family: BL00211: I505-L516, L1389-D1420 ABC transporters family: DM00008 P41233 839-1045:K1268-M1462, I471-P600, E587-N641 DM00008 P34358 611-816:F1262-M1462, I471-D592, E585-N641 DM00008 P41233 1851-2058:K1266-S1464, I471-V584, V588-N641 DM00008 P23703 41-246:K1268-G1465, V476-L609, E585-G642	HMMER HMMER-PFAM ProfileScan MOTIFS BLIMPS-BLOCKS BLAST-DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6	6754139CD1	382	S124 S260 S340 S85 T337		Transmembrane domains: A168-H191, V200-L217, Y233-N253, F361-L378 Neurotransmitter-gated ion channel: D2-L378 Neurotransmitter-gated ion-channels signature: V66-G120 Neurotransmitter-gated ion channel: C86-C100 Neurotransmitter-gated ion channel: BL00236:M1-D26, Y155-S196, V43-N52, D71-H109 Neurotransmitter-gated ion channel: PR00252:T9-W25, L42-K53, C86-C100, L162-N174 Nicotinic acetylcholine channel: PR00254:M1-L12, Y30-W44, I48-G60, V66-S84 Neurotransmitter-gated ion channel: DM00195 P43144 5-478:M1-E296, R323-A381 DM00195 JH0173 14-503:M1-P314, L327-A381 DM00195 P09478 5-538:R4-L297, E296-A381 DM00195 P54131 3-491:M1-A312, L327-A381 Postsynaptic ion channel: PD000153: M1-R262, S298-V377	HMMER HMMER-PFAM ProfileScan MOTIFS BLIMPS-BLOCKS BLIMPS-PRINTS BLIMPS-PRINTS BLAST-DOMO BLAST-PRODOR

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
7	6996659CD1	1115	S110 S202 S1030 S248 S303 S1080 S317 S334 T1101 S383 S448 S1098 S5 S552 T1109 S563 S800 S801 S809 S976 S986 T441 T519 T636 T693 T704 T741 T796 T85 T949 T997 Y1106	N145 N264 N275 N285 N296 N426 N439 N549 N565 N709 N886 N965 N984 N1015 N1018 N1069	Signal peptide: M1-V24 Signal peptide: M1-S33 Transmembrane domains: M677-T693, F931-I946 Ligand-gated ion channel: H674-E952 ATP/GTP binding site: G373-T380 NMDA receptor signature: PR00177:M677-G702, F744-E771, F931-V955, F593-L621 Glutamate receptor: DM00247 P35436 615-886: T731-Q993 DM00247 Q03391 640-919: T731-Y956 DM00393 Q01097 377-614: G482-F728 DM00247 Q01097 616-887: T731-Y956 Ionotropic glutamate receptor: PD156309: S170-Y577 PD139812: M1-P169 PD124284: S986-S1115 PD000500: M670-E952 Signal peptide: M1-A41 Transmembrane domains: F95-L114, V167-F187 Transmembrane domains: G23-A43, F103-I122, L132-D150, F337-Q359	HMMER SPScan HMMER HMMER-PFAM MOTIFS BLIMPS-PRINTS BLAST-DOMO BLAST-PRODOM SPScan HMMER HMMER
8	7472747CD1	295	S193 S199 S91 T59	N57 N86		
9	7474121CD1	384	S205 S252 S267 S42 T306 T329 T74	N70 N96		

Table 3 (cont.)

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
10	7475615CD1	769	S200 S3 S407 S461 S475 S572 S651 S707 S738 S742 S748 S87 T15 T282 T60 Y470 Y57	N195 N198 N596	Transmembrane domains: F245-I265, N294-V311, F491-V510 Sulfate transporter family: L229-T513 Sulfate transporters profile: BL01130: G119-V172, T217-L268 Sulfate transporter: DM01229 P40879 5-462: R49-V456 DM01229 P50443 49-505: E67-P495 DM01229 P45380 10-468: K78-S485 DM01229 Q02920 1-447: S87-I481 Sulfate transporter protein: PD001121: V93-T197 PD001755: H641-R720, L521-D579	HMER HMER-PFAM BLIMPS-BLOCKS BLAST-DOMO BLAST-PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
11	7475656CD1	882	S102 S108 S13 S324 S360 S394 S395 S518 S544 S591 T190 T242 T649 T754 T799 T869 Y240 Y529	N330 N640 N770 N8	Transmembrane domains: L139-F159, T242-L258, I366-L392 Transmembrane region cyclic nucleotide domain: Y209-I453 Cyclic nucleotide-binding domain: K482-M570 Cyclic nucleotide-binding domain: I494-I515 Cyclic nucleotide-binding site: BL00888: G491-V514, G527-L536 Cyclic nucleotide-binding domain: DM01165 A55251 333-706: H302-E576 DM01165 P29973 311-684: H302-E576 DM01165 Q03041 286-658: H302-E576 DM01165 S52072 262-635: H302-R572 Cyclic nucleotide gated hyperpolarization activated cation channel: PD079330: P747-L882 PD089437: A627-M722 PD108745: M1-D62 PD151315: T577-Q626	HMMER HMMER-PFAM HMMER-PFAM MOTIFS BLIMPS-BLOCKS BLAST-DOMO BLAST-PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
12	7480632CD1	1547	S134 S196 S1102 S216 S395 T1301 S7 T1343 T1389 S723 S742 T1372 S754 S779 S1405 S787 S883 T1449 S891 T107 T1535 T377 T448 S1158 T493 T551 T1212 T574 T682 S1218 T700 T715 T1219 T775 T791 S1252 T810 T86 S1275 T936 T975 S1283 Y915 S462 T1421 Y1144	N194 N71 N84 N879 N880 N908 N958 N1100 N1228	Transmembrane domains: I274-V294, I305-I324, M328-L349, I399-F419, I824-M843, M946-I963, L1021-F1040, L1046-L1064, D1105-F1123 ABC transporter: G509-G651, G1236-G1420 ABC transporters family signature: L1327-D1375 ATP/GTP binding sites: G516-S523, G1243-S1250 ABC transporters family: BL00211: I514-I525, L1344-D1375 ABC transporters family: DM00008 P41233 839-1045:K1223-M1417, I480-P609, E596-N650 DM00008 P41233 1851-2058:R1220-S1419, I480-V593, V597-N650 DM00008 P34358 611-816:F1217-M1417, I480-D601, E594-N650 DM00008 P23703 41-246:K1223-G1420, V485-L618, E594-G651	HMMER HMMER-PFAM ProfileScan MOTIFS BLIMPS-BLOCKS BLAST-DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
13	6952742CD1	698	S278 S355 S367 S446 S464 S594 S676 T114 T523 T559 T626 T667 T683 Y519	N155 N160	SULFATE TRANSPORTERS: DM01229 P45380 10-468: V15-R462 do TRANSPORTER; SULFATE; DM08211 P45380 470-702: M463-L698 PROTEIN TRANSPORT SULFATE TRANSPORTER TRANSMEMBRANE PERMEASE INTERGENIC REGION AFFINITY GLYCOPROTEIN PD001255: L285-L498 SULFATE TRANSPORTER TRANSPORT PROTEIN TRANSMEMBRANE GLYCOPROTEIN AFFINITY SULPHATE HIGH PERMEASE PD001121: L49-R136 SULFATE TRANSPORTER PROTEIN TRANSPORT TRANSMEMBRANE AFFINITY GLYCOPROTEIN SULPHATE HIGH DISEASE PD001755: H607-R689, A508-F551 SULFATE ANION TRANSPORTER 1 CANALICULAR SULFATE/CARBONATE ANTIPORTER TRANSPORT TRANSMEMBRANE GLYCOPROTEIN PD083148: D135-L191 Sulfate transporters proteins BL01130: A180-V231, D72-L125 Transmembrane domain: E67-Y87, L411-A428 Sulfate transporter family Sulfate_transp: M192-T502 Sulfate_Transporter: P95-R116	BLAST-DOMO BLAST-DOMO BLAST-PRODROM BLAST-PRODROM BLAST-PRODROM BLAST-PRODROM BLIMPS-BLOCKS HMMER HMMER-PFAM MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14	7478795CD1	766	S161 S275 S28 S33 S354 S46 S543 S571 S595 S671 S702 S763 T139 T153 T181 T209 T311 T367 T377 T512 Y602	N280 N508 N524 N599 N761	<p>MALK PROTEIN: DM00130 S13426 168-477: L195-G502</p> <p>ATP-BINDING TRANSPORT PROTEIN TRANSMEMBRANE GLYCOPROTEIN TRANSPORTER MULTIDRUG RESISTANCE ABC GLYCOPROTEIN PD000130: V229-L455</p> <p>ATP-BINDING TRANSPORT TRANSMEMBRANE REGION PD00131:G283-D292, S543-I596, K691-L728</p> <p>Transmembrane domain: V85-F104, V185-F204, L328-G347, Y411-G431</p> <p>ABC transporter transmembrane region. ABC_membrane: L188-M459</p> <p>ABC transporter ABC_tran: G532-G716</p> <p>Abc_Transporter: L643-L657</p> <p>ATP/GTP-binding site motif A (P-loop) Atp_Gtp_A: G539-S546</p> <p>ABC transporters family signature atp_bind_transport.prf: I625-D674</p>	<p>BLAST-DOMO</p> <p>BLAST-PRODOM</p> <p>BLIMPS-PRODOM</p> <p>HMMER</p> <p>HMMER-PFAM</p> <p>HMMER-PFAM</p> <p>MOTIFS</p> <p>MOTIFS</p> <p>PROFILES CAN</p>

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
15	656293CD1	450	S153 S192 S328 S408 T405	N40 N56	NEUROTRANSMITTER-GATED ION-CHANNELS DM00195 P43144 5-478:A25-E364, R391-A449 CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153:S131-R361 Neurotransmitter-gated ion channel BL00236:D139-H177, Y223-S264, V57-D94, V111-N120 NEUROTRANSMITTER-GATED Ion Channel PR00252:T77-W93, L110-K121, C154-C168, L230-N242 NICOTINIC ACETYLCHOLINE RECEPTOR SIGNATURE PR00254:V134-S152, S64-L80, Y98-W112, I116-G128 signal peptide: M1-G24 transmembrane domain: A236-H259, V268-L285, Y301-N321, F429-L446 Neurotransmitter-gated ion-channel neur_chan:A30-L446 Neurotr_Ion_Channel C154-C168 Neurotransmitter-gated ion-channels signature neurotr_ion_channel.prf:V134-G188 signal_cleavage: M1-G24	BLAST_DOMO BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS HMMER HMMER HMMER_PFAM MOTIFS PROFILES SCAN SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16	7473957CD1	260	S114 S12 S211 T136 T227 T28 T47 T49 T63 T84	N215 N216	EUKARYOTIC MITOCHONDRIAL PORIN DM01893 P45879 1-282:S12-A260 PORIN CHANNEL VOLTAGEDEPENDENT OUTER MEMBRANE PROTEIN MITOCHONDRION ANIONSELECTIVE MITOCHONDRIAL VDAC PD003211:A15-Q259 Eukaryotic mitochondrial porin BL00558:G33-L46, T57-S81 EUKARYOTIC PORIN SIGNATURE PR00185:G45-T60, E124-E135, Y224-D241 Eukaryotic porin Euk_porin:A5-A260 Eukaryotic_Porin Y202-Y224 Eukaryotic mitochondrial porin signature eukaryotic_porin.prf:M16-S81	BLAST_DOMO BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PRINTS HMMER_PFAM MOTIFS PROFILES SCAN
17	7474111CD1	506	S187 S194 S2 S231 S286 S423 S493 S57 T241 T273 T357 T385	N284	do CHANNEL; POTASSIUM; CDRK; FORM; DM00436 JH0595 144-307:P230-I366 CHANNEL IONIC PROTEIN POTASSIUM SUBUNIT VOLTAGEGATED TRANSMEMBRANE CALCIUM TRANSPORT ION PD000141:F319-Y486 POTASSIUM CHANNEL SIGNATURE PR00169:F319-V339, M363-C389, E392-E415, F427-M449, G456-F482, E211-P230, P245-T273, I293-K316 transmembrane domain: I253-C270, V356-A373, V394-L413 Ion transport protein ion_trans:I263-I478	BLAST_DOMO BLAST_PRODUM BLIMPS_PRINTS HMMER HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
18	7480826CD1	506	S12 S22 S280 S320 T125 T181 T276 T349 T433	N254 N258 N27 N274 N278 N326 N79	TRANSPORTER PROTEIN PD138374:H360-H506 ACID AMINO PROTEIN TRANSPORTER PERMEASE TRANSMEMBRANE INTERGENIC REGION PUTATIVE PROLINE PD001875:S76-I394 transmembrane domain: A97-L116, L224-V243, L192-S210, I330-T349, V375-F392, I416-I441, I473-I493 Transmembrane amino acid transporter protein Aa_trans:A95-S489	BLAST_PRODOM BLAST_PRODOM HMMER HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
19	6025572CD1	315	S53 T209 T245		MITOCHONDRIAL ENERGY TRANSFER PROTEINS DM00026 S31935 110-208:Q120-K218 MITOCHONDRIAL ENERGY TRANSFER PROTEINS DM00026 P02722 11-96:L25-L110 PROTEIN TRANSPORT TRANSMEMBRANE REPEAT MITOCHONDRION CARRIER MEMBRANE INNER MITOCHONDRIAL ADP/ATP PD000117:S18-V210 Mitochondrial energy transfer proteins BL00215:L25-Q49, I271-G283 MITOCHONDRIAL CARRIER PROTEINS PR00926:A229-M251, D23-T36, T36-V50, G85-D105, T138-D156, Y186-F204 ADENINE NUCLEOTIDE TRANSLOCATOR PR00927:F20-A32, Y63-R84, T96-K108, R123-G136, R164-L185, S225-Y241, E275-R290 Mitochondrial carrier proteins mito_carr:S19-F308 Mitoch_Carrier: P40-L48, P145-L153, P242-M250 Mitochondrial energy transfer proteins signature mitoch_carrier.prf:F20-I73, F125-I176, F222-I271	BLAST_DOMO BLAST_DOMO BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS HMMER_PFAM MOTIFS PROFILESCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
20	5686561CD1	540	S162 S180 S24 S29 S327 S349 S454 T527	N399 N406	Transmembrane domains: A77-Y100, Y220-L243, I259-L285, V291-Y311, A369-F389 Sodium channel signature: PR00170:G362-F389, Y76-G105, L361-F389, K109-G134 Calcium channel: DM00043 A55645 1137-1259: A250-V298 (P-value = 2.7e-5) Voltage gated calcium channel PD000032:Y221-G391, I460-F486, N423- W443 (P-value = 1.1e-6)	HMMER BLIMPS-PRINTS BLAST-DOMO BLAST-PRODOR
21	1553725CD1	322	S142 S217 S295 S39 T133 T168 T304 T62 Y315	N123 N131 N29	PROTEIN TRANSMEMBRANE CHROMOSOME PUTATIVE TRANSPORTER C17G6.15C TRANSPORT XV READING FRAME PD006986:F8-L253	BLAST_PRODOR

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
22	1695770CD1	417	S108 S122 S163 S43 S56 T196 T239 T243 T410 T411 T88	N72	Signal peptide: M1-A28 Transmembrane domains: M255-I279, I320-I339 Neurotransmitter-gated ion-channel domain: P44-F341 Neurotransmitter-gated ion channels signature BL00236: V73-R110, I127-N136, N157-Y195, F242-A283 Neurotransmitter-gated ion-channels signature: L152-E206 Neurotransmitter-gated ion-channel family signature PR00252:R93-Y109, S126-E137, C172-C186, F249-Q261 Gamma-aminobutyric acid A (GABAA) receptor signature PR00253:Y258-W278, A284-S305, I318-I339 CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: R99-K347 NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 S18836 18-453: R24-D417 Neurotransmitter-gated ion channel motif: C172-C186	HMMER HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLIMPS_PRINTS BLIMPS_PRINTS BLAST_PRODOR BLAST_DOMO MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
23	4672222CD1	1864	S103 S195 S196 S2 S22 S406 S5 S547 S697 S727 S757 S836 S87 S883 T115 T12 T299 T318 T349 T367 T508 T523 T529 T593 T603 T615 T675 T778 T795 T842 Y327 S1476 S1503 T1163 S1191 S1361 S1413 T1430 S1493 S1526 S1555 S1614 T1631 S1633 T1742 T1758 S1850 T1245 S1410 S1456 T1471 S1499 S1698 S1859 Y1220 Y1552	N404 N550 N715 N718 N805 N925 N1058 N1465 N1466 N1595 N1773 N1849	Transmembrane domains: F858-M878, N999-L1022, V1079-Q1102 PROTEIN MELASTATIN CHROMOSOME TRANSMEMBRANE C05C12.3 T01H8.5 I F54D1.5 IV PD018035:Y108-L439 PD039592:E597-N801 PD151509:V974-P1063, W1030-K1253 PD022180:W434-R545	HMMER BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
24	6176128CD1	1237	S102 S135 S139 S168 S179 S361 S407 S438 S439 S538 S686 S690 S713 S720 S726 S770 S808 S871 S9 S924 S93 S954 T156 T302 T351 T391 T446 T517 T609 T718 T77 T994 S1090 S1098 S1219 S1013 S1030 T1146 T1155 T1190 T1231 S1125 S1215 S1221	N100 N133 N137 N279 N343 N584 N607 N682 N933 N1153	Transmembrane domains: M155-Y177, M248-F264, L310-L330 CHANNEL POTASSIUM IONIC CALCIUMACTIVATED ALPHA CALCIUM SUBUNIT ACTIVATED PROTEIN LARGE PD003090:R337-F629, I784-M889, L926-P983, Y1003-E1033, Q1176-S1215 do CHANNEL; POTASSIUM; MSLO; ACTIVATED; DM05442 A48206 351-1123: R337-F618, P944-P983, Q1176-S1226	HMMER BLAST_PRODUM BLAST_DOMO
25	7473418CD1	539	S299 S321 T535 S1221	N533	Transmembrane domains: V15-C38, C50-F67, F264-F282, A323-R341 Sodium:sulfate symporter signature: BL01271:S451-I505, T132-I151, M216-V240, P378-G399 PROTEIN TRANSMEMBRANE TRANSPORT MEMBRANE INNER TRANSPORTER SODIUM SYMPORT OF COTRANSPORTER PD000549:V15-V173, M216-W518 do RENAL; BOUND; PRO-SER-ALA; NA; DM02914 S43561 28-507:R37-M159, P199-W349, L367-T517	HMMER BLIMPS_BLOCKS BLAST_PRODUM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
26	7474129CD1	755	S339 S353 S367 S463 S53 S572 S589 S653 S732 T128 T132 T255 T270 T277 T300 T343 T358 T362 T37 T376 T441 T664 Y225 Y347 Y587	N417 N648 N735	Transmembrane domains: V490-F507, L556-L573, P616-M642 Ank repeat: E179-K211, F226-S259, D305-K333 VANILLOID RECEPTOR SUBTYPE 1 PD101189: Q52-L291 PROTEIN OLFACTORY CHANNEL B0212.5 T09A12.3 T10B10.7 VANILLOID RECEPTOR SUBTYPE F28H7.10 PD011151:N303-E430 Transmembrane domain: L212-V230 Mitochondrial carrier proteins domain: Q8-M294 Mitochondrial energy transfer proteins signature: BL00215:L214-Q238, V256-G268 Mitochondrial energy transfer proteins signature: A10-G59, L107-I160, K204-A276, K213-N259 PROTEIN TRANSPORT TRANSMEMBRANE REPEAT MITOCHONDRION CARRIER MEMBRANE INNER MITOCHONDRIAL ADP/ATP PD000117: Y44-S241 Mitochondrial carrier protein motifs: P126-L134 P229-I237	HMMER HMMER_PFAM BLAST_PRODOR BLAST_PRODOR HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLAST_PRODOR MOTIFS
27	7481414CD1	301	S143 S203 S290 T136 T32			

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
28	7481461CD1	515	S10 S104 S163 S257 S272 S277 S4 S474 S511 S97 T233 T250 T484	N81	Transmembrane domains: V117-F135, Y169-L191, I190-I215, G229-F245, I376-F395 Monocarboxylate transporter domain: A77-A455	HMMER
					XLINKED PESTCONTAINING TRANSPORTER SOLUTE CARRIER FAMILY MONOCARBOXYLIC ACID TRANSPORTERS MEMBER PD030892:P33-V111 do PEST; TRANSPORTER; LINKED; DM05037 P36021 155-612:E63-M489	HMMER_Pfam BLAST_PRODOR BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
29	7472541CD1	1519	S223 S307 S432 S456 S472 S486 S498 S510 S538 S579 S628 S63 S648 S668 S701 S728 S732 S741 S756 S779 S826 S832 S903 S912 S986 T275 T341 T437 T449 T466 T495 T563 T597 T664 T674 T716 T73 T755 T805 T880 T945 T961 S1509 S1110 S1131 T1198 S1256 S1278 T1431 S1480 S1406 T1439 S1505 Y1079	N148 N298 N339 N354 N41 N51 N69 N991 N1249 N1331	Transmembrane domains: M313-G331, L358-L383, L1317-C1337 E1-E2 ATPase domains: E422-V444, L935-H985 E1-E2 ATPases phosphorylation site BL00154:G173-L190, I427-F445, D949-L989 E1-E2 ATPases phosphorylation site: I413-A461 P-type cation-transporting ATPase PR00119:F431-F445, A965-D975, I1111-I1130 ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATPBINDING PROTEIN PROBABLE CALCIUMTRANSPORTING CALCIUM TRANSPORT PD004657:A1145-F1374 PD006317:Y162-E255 PD149930:C1085-F1144 PD004932:R65-P121 do ATPASE; CALCIUM; TRANSPORTING; DM02405 P32660 318-1225:R157-E475, E776-N1209 E1-E2 ATPase motif: D433-T439 ATP/GTP binding site (P-loop): G1053-T1060	HMMER HMMER_Pfam BLIMPS_BLOCKS PROFILES SCAN BLIMPS_PRINTS BLAST_PRODOR BLAST_DOMO MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
30	6999183CD1	1585	S2, S7, T30, S61, S70, T86, S114, S198, T267, T459, T464, T576, S626, T717, T744, S756, T757, S779, S789, T793, S885, S893, Y917 S924, T938, T967, T971, S1005, S1054, S1097, S1158, S1202, S1262, T1267, T1296, T1339, T1381, T1410, T1427, T1431, S1457, Y1544, S1574, S1549,	N72, N121, N196, N245, N457, N546, N557, N881, N910, N960, N1272, N1337	ABC TRANSPORTERS FAMILY: DM00008 P41233 839-1045: I1268-M1455, I482-P611, E598-N652 ABC transporters family: BL00211: L516-L527, L1382-D1413 Transmembrane domain (transmem_domain): I1058-L1082, I1099-L1117, G1124-I1147, L1167-M1193, T30-F48, T224-V242, W271-I289, T306-I326, P329-L346, F358-M375, Y398-Y420, V1034-F1053 ABC transporter (ABC_tran): G511-G653, G1280-G1458 ATP/GTP-binding site motif A (P-loop) (Atp_Gtp_A): G518-T525, G1287-S1294 ABC transporters family signature (atp_bind_transport.prf): I1362-D1413	BLAST-DOMO BLIMPS-BLOCKS HMMER HMMER-PFAM MOTIFS PROFILES CAN

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
31	2194064CB1	1129	1071-1129, 833-898	g5110579	1	485
				FL2194064_g770598_000019_g7 670446	203	1129
				6542780F9 (LNODNON02)	32	481
				FL097646_00001	431	2542
32	2744094CB1	2699	1-2196, 2541-2587	55058921H1	1	793
				70317743D1	2347	2699
				70317681D1	2209	2639
				71911330V1	5832	6369
33	2798241CB1	6369	1-1210, 1759-5012	70300809D1	5128	5690
				6340750H1 (BRANDIN01)	5650	6322
				7601441J1 (ESOGTME01)	4623	5186
				6314138H1 (NERDTN03)	5235	5750
				7690596H1 (PROSTME06)	4145	4636
				7753104J1 (HEAONOE01)	5764	6357
				4013186F9 (MUSCNOT10)	3758	4391
				7606344H1 (COLRTUE01)	1764	2219
				6913644H1 (PITUDIR01)	4608	5181
				55052455J1	1981	2827
				7400061H1 (SINIDME01)	1	502
				2798241T6 (NPOLNOT01)	1325	1955
				55058989J1	2548	3298
				7100413F7 (BRAWTDRO2)	483	1185
34	3105257CB1	2558	1-587, 2435-2558	6744456H1 (BRAFNOT02)	568	1274
				55053647J1	3011	3823
				6586921H1 (TLYMUNT03)	1157	1724
				70864718V1	1864	2353
				70549000V1	1608	2310
				FL3105257CT1_00001 6451207H1 (BRAINOC01)	1	1843
					1868	2558

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
35	3200979CB1	5065	5030-5065, 1-3313	FL3200979_g3810670_g4240130 71698878V1	1 4463	4779 5065
36	6754139CB1	1677	1-686	656293H1 (EOSINOT03) 55062573H1 GBI:edit GNN:g8017750_000028_004 g5678193 6754139J1 (SINTFER02)	532 789 1 386 684 684	800 875 531 1677 883 874
37	6996659CB1	3714	1-1916, 3071-3091, 2092-2619	6996659F8 (BRAXTDRI17) GBI.g9211864_01_04_05_12.edi t 55098348H2 1596150T6 (BRAINOT14) 7124651F6 (COLNDIY01) g4622477 1596150F6 (BRAINOT14) 55063531J1 7291716R6 (BRAIFER06) 7291716F6 (BRAIFER06) 55063924J1	1180 1303 2752 3116 2605 3322 2967 1 510 219 1768	1915 3006 2942 3707 2776 3714 3466 309 1209 1174 1994
38	7472747CB1	1009	1-388, 571- 704, 778- 1009	FL7472747_g6983242_000026_g3 925427 7616162H1 (COLNTUN03)	122 1	1009 450
39	7474121CB1	1155	1-1155	GNN.g7259672_000014_002	1	1155
40	7475615CB1	2733	1852-2185, 1484-1579, 665-1340, 1-249, 2334-2733, 454-495	FL7475615_g8980204_000002_g2 654005_1_11-12 FL7475615_g8980204_000002_g2 654005_1_6-7 FL7475615_g8980204_000002_g2 654005_1_12-13	1580 986 1687	1756 1221 1849

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
41	7475656CB1	3457	3284-3346, 1169-1646, 1-290, 2835-2868, 2018-2292, 3030-3174, 780-844, 456-653	FL7475615_g8980204_000002_g2	1139	1369
				654005_1_7-8		
				55092029J1	341	1088
				55083049H1	1	470
				1509180F6 (LUNGNOT14)	1744	2228
				FL7475615_g8980204_000002_g2	1222	1483
				654005_1_8-9		
				GNN.g7342135_000012_002	821	1579
				6806177J1 (SKIRNOR01)	1995	2733
				FL7475615_g8980204_000002_g2	1484	1686
				654005_1_10-11		
				55073909H2	1	110
				g3168873_CD	382	2628
				7946572H1 (BRABNOE02)	228	536
42	7480632CB1	5622	1-3676, 5557-5622	5373417T9 (BRAINOT22)	2245	2901
				GNN.g6532090_000006_000019.e	43	867
				dit		
				2428507R6 (SCORNON02)	2911	3457
				5373417F8 (BRAINOT22)	1396	1620
				5893974H1 (BRAYDIN03)	2879	3160
				4787380H1 (BRATNOT03)	1461	1717
				1450339F1 (PENITUT01)	4134	4646
				7270152H1 (OVARDIJ01)	167	646
				71697049V1	4737	5460
				3488927H1 (EPIGNOT01)	2908	3106
				6774619J1 (OVARDIR01)	2052	2720
				5063703F6 (ARTFTDT01)	4886	5622
				55072886J1	3675	4262
				GBI.g3810670_000001.edit	266	4674
				6488228F9 (MIXDUNB01)	1	632
				7670233H2 (BONRNOC01)	4317	4878

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
43	6952742CB1	2600	2329-2600, 1-224, 1190-1560, 1957-2046, 1006-1030	5884027F8 (LIVRN08)	2088	2600
				55063579H1	779	1276
				GBI:g7232144_000013.edit.3	1626	2351
				6816048H1 (ADRETUR01)	1	316
				6952742H1 (BRAITDR02)	1140	1824
				GNN.g6970605_000013_002	342	1355
44	7478795CB1	2917	2698-2917, 1808-2065, 398-714, 923-976	GBI:g7232144_000013.fasta.ed it	255	506
				72016954V1	2193	2917
				71989431V1	2165	2912
				72017820V1	1369	2155
				72017055V1	1160	2053
				72017371V1	570	1212
				72017076V1	1958	2859
				72017430V1	476	1146
				55076285H1	1	566
				GBI.g8017750_edit	1	1353
45	656293CB1	1474	1-362	FL656293_g8017750_000028_g67	130	895
				46563_2_2-3		
				FL656293_g8017750_000028_g67	363	1353
				46563_2_3-4		
46	7473957CB1	1742	1-367, 1680-1742	7675576H1 (NOSETUE01)	907	1474
				4648731F9 (PROSTUT20)	610	1274
				71166638V1	1	610
				71165785V1	1010	1742
				6830443J1 (SINTNOR01)	592	1266
47	7474111CB1	2312	1-639, 1686-1712, 2004-2312, 1860-1908	7761487H1 (THYMNOE02)	6	632
				6770140H1 (BRAUNOR01)	1692	2312
				7761487J1 (THYMNOE02)	1	506
				GNN.g7243948_CDS_1	183	1845

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
48	7480826CB1	2320	161-224, 2044-2320	7752763J1 (HEAONOE01)	1668	2320
				60143671D1	467	917
				6052064J1 (BRABDIR03)	1080	1658
				6484950H1 (MIXDUNB01)	1276	1723
				2944045H1 (BRAITUT23)	827	1118
				7469461H1 (LUNGNOE02)	1	498
49	6025572CB1	1781	1-170	FL6025572_g7382154_000015_g1	347	1063
				197164		
				4923834H1 (TESTNOT11)	1	291
				g3838735	1313	1781
				g3734777	252	472
				71970611V1	1285	1780
				6025572F6 (TESTNOT11)	883	1627
				71412362V1	1088	1702
				6060785H1 (BRAENOT04)	551	1100
				7695065J1 (LNODTUE01)	387	1052
50	5686561CB1	2433	1-1078, 1197-1275	7633409H1 (SINTDIE01)	1	483
				3776733H1 (BRSTNOT27)	2148	2433
				2802364F6 (PENCNOT01)	1765	2304
				5564984F6 (TLYMNOT08)	860	1528
				70730430V1	1525	2108
				60211064U1	344	823
				72050509V1	1176	1772
				70300327D1	984	1428
				70300706D1	1	262
				1553725X15C1 (BLADTUT04)	54	694
51	1553725CB1	1772	1571-1772	70300332D1	729	1286
				55117454H1	1155	1874
				55110123H1	286	1179
				55072985J1	1	542
52	1695770CB1	1874	1-479, 1298-1874, 1131-1216, 886-984			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
53	4672222CB1	6211	3238-3683, 4625-4798, 2313-2462, 1-1636	55047368J1	1925	2815
				71007436V1	5663	6211
				71998604V1	4613	5344
				71995592V1	3913	4598
				3462433F7 (293TF2T01)	2738	3162
				71997753V1	4522	5239
				71995863V1	3346	3886
				55073038H1	818	1499
				55141177J1	2942	3318
				71998657V1	3811	4537
				6141577F6 (BMARTXT03)	1	878
				55140386J1	1086	1915
				GBI:g8189326.edit	2957	3903
				5092011F6 (UTRSTMR01)	1797	2436
				7743692H1 (ADRETUE04)	5374	5927
				2505959F6 (CONUTUT01)	5325	5866
				GBI.g979669_000005_000004.ed it	1	1143
54	6176128CB1	3714	1-197, 329- 2513, 3301- 3336	6859776H1 (BRAIFEN08)	2265	2953
				GBI.g979669_000002.edit	3612	3714
				GBI.g7739135_000005.edit	3115	3711
				6772216J1 (BRAUNOR01)	2991	3324
				6887873J1 (BRAITDR03)	899	1503
				8039114H1 (SPLNNOE01)	1741	2374
				6907605J1 (PITFDIR01)	2586	3088
				6445788H2 (BRAINOC01)	1383	2006
				6891702F6 (BRAITDR03)	543	1053
				7065904R6 (BRATNOR01)	383	645
				FL7473418_g3176728_g5531902_ 1_4-5	369	740
				7056016H1 (BRALNON02)	2658	3115
55	7473418CB1	3115	1-1411			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
56	7474129CB1	2846	1-1696, 2073-2846, 1777-2012	FL7473418_g3176728_g5531902_ 1_7-8	864	1188
				1324158F6 (LPARNOT02)	2114	2695
				6899347H1 (LIVRTMR01)	1074	1568
				FL7473418_g3176728_g5531902_ 1_5-6	548	863
				70075691U1	2291	2782
				FL7473418_g3176728_g5531902_ 1_6-7	739	1069
				FL7473418_g3176728_g5531902_ 1_1-2	1	231
				FL7473418_g3176728_g5531902_ 1_10-11	1351	1620
				FL7473418_g3176728_g5531902_ 1_2-3	103	368
				7114876H1 (BRAENOK01)	1549	1954
				FL7473418_g3176728_g5531902_ 1_3-4	232	547
				4895008F6 (LIVRTUT12)	1752	2240
				55109928H1	2480	2846
				55109306J1	1837	2660
57	7481414CB1	906	441-541, 262-348	55124533H1	1	832
				55124525H1	1073	1893
				55073088J1	796	1208
				GBI.g9454493_000005_000056.e dit	1	906

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
58	7481461CB1	1840	1-91	70481006V1	551	1137
				70465445V1	673	1250
				1748722F6 (STOMTUT02)	1423	1840
				60266587D1	1225	1801
				7637372J1 (SINTDIE01)	221	642
				g5933739	1	407
				6772907J1 (BRAUNOR01)	1641	2204
59	7472541CB1	5348	1384-1560, 1-1188, 4239-4906, 2145-2970, 4944-5348	2182261F6 (SININOT01)	4301	4634
				5459667H1 (SINITUT03)	3276	3550
				GNN.g7710567_000006_002.edit	1057	2001
				7362215H1 (BRAIFEE05)	1	526
				GNN.g7708823_000019_002	4306	4862
				7032970H1 (BRAXTDR12)	2692	3426
				7313608H1 (BRABDIE02)	731	1260
				71462931V1	4732	5348
				5767060H1 (STOMFET02)	3887	4428
				8069315J1 (BRAIFEE05)	91	792
				7582660H1 (BRAIFEC01)	3510	4131
				GNN.g7454125_000004_002.edit	1382	3918
				6772907H1 (BRAUNOR01)	2476	2994
				GBI.g3873182_000001.edit5p	1	3167
60	6999183CB1	5149	1-1797, 4753-4852, 3028-3711, 2471-2667	72017145V1	4087	4903
				6999183R8 (HEALDIR01)	384	1128
				55051672H1	909	1573
				72017349V1	3836	4767
				72293922V1	2616	3434
				55144835H1	2154	2939
				55144834J1	3263	3947
				55076606J1	1126	1592
				72017610V1	4219	5149

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
31	2194064CB1	THYRTUT03
32	2744094CB1	BRSTTUT15
33	2798241CB1	PROSTME06
34	3105257CB1	BLADNOT01
35	3200979CB1	PENITUT01
36	6754139CB1	BRSTNOR01
37	6996659CB1	BRAIFER06
38	7472747CB1	COLNTUN03
40	7475615CB1	LUNGNON07
41	7475656CB1	BRAINOT22
42	7480632CB1	PENITUT01
43	6952742CB1	LIVRNON08
44	7478795CB1	BRAENOT02
45	656293CB1	COLNNOT22
46	7473957CB1	BRAHTDR03
47	7474111CB1	THYMN0E02
48	7480826CB1	MIXDUNB01
49	6025572CB1	TESTNOT11
50	5686561CB1	BRAENOT04
51	1553725CB1	THYMNON04
52	1695770CB1	COLNNOT23
53	4672222CB1	PITUDIR01
54	6176128CB1	BRAITDR03
55	7473418CB1	LPARNOT02
56	7474129CB1	PLACNOT05
58	7481461CB1	OVARTUT05
59	7472541CB1	BRAIFEE05
60	6999183CB1	HEALDIR01

Table 6

Library	Vector	Library Description
BLADNOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the bladder tissue of a 78-year-old Caucasian female, who died from an intracranial bleed. Patient history included basal cell carcinoma, arthritis, and chronic hypertension.
BRAENOT02	pINCY	Library was constructed using RNA isolated from posterior parietal cortex tissue removed from the brain of a 35-year-old Caucasian male who died from cardiac failure.
BRAENOT04	pINCY	Library was constructed using RNA isolated from inferior parietal cortex tissue removed from the brain of a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomeningeal fibrosis and multiple microinfarctions of the cerebral neocortex. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly and an enlarged spleen and liver.
BRAHTDR03	PCDNA2.1	This random primed library was constructed using RNA isolated from archaocortex, anterior hippocampus tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
BRAIFEE05	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation.
BRAIFER06	PCDNA2.1	This random primed library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation. Serologies were negative.

Table 6 (cont.)

Library	Vector	Library Description
BRAINOT22	pINCY	Library was constructed using RNA isolated from right temporal lobe tissue removed from a 45-year-old Black male during a brain lobectomy. Pathology for the associated tumor tissue indicated dysembryoplastic neuroepithelial tumor of the right temporal lobe. The right temporal region dura was consistent with calcifying pseudotumor of the neuraxis. Family history included obesity, benign hypertension, cirrhosis of the liver, obesity, hyperlipidemia, cerebrovascular disease, and type II diabetes.
BRAITDR03	PCDNA2.1	This random primed library was constructed using RNA isolated from allocortex, cingulate posterior tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
BRSTNOR01	pINCY	Library was constructed using RNA isolated from diseased breast tissue removed from a 59-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive lobular carcinoma with extension into ducts. Patient history included cirrhosis, esophageal ulcer, hyperlipidemia, and neuropathy.
BRSTTUT15	pINCY	Library was constructed using RNA isolated from breast tumor tissue removed from a 46-year-old Caucasian female during a unilateral extended simple mastectomy.. Pathology indicated invasive grade 3, nuclear grade 2 adenocarcinoma, ductal type. An intraductal carcinoma component, non-comedo, comprised approximately 50% of the neoplasm, including the lactiferous ducts. Angiolymphatic involvement was present. Metastatic adenocarcinoma was present in 7 of 10 axillary lymph nodes. The largest nodal metastasis measured 3 cm, and focal extracapsular extension was identified. Family history included atherosclerotic coronary artery disease, type II diabetes, cerebrovascular disease, and depressive disorder.

Table 6 (cont.)

Library	Vector	Library Description
COLNNOT22	pINCY	Library was constructed using RNA isolated from colon tissue removed from a 56-year-old Caucasian female with Crohn's disease during a partial resection of the small intestine. Pathology indicated Crohn's disease of the ileum and ileal-colonic anastomosis, causing a fistula at the anastomotic site that extended into pericolic fat. The ileal mucosa showed linear and punctate ulcers with intervening normal tissue. Previous surgeries included a partial ileal resection and permanent ileostomy. Family history included irritable bowel syndrome in the mother and the siblings.
COLNNOT23	pINCY	Library was constructed using RNA isolated from diseased colon tissue removed from a 16-year-old Caucasian male during a total colectomy with abdominal/perineal resection. Pathology indicated gastritis and pancolitis consistent with the acute phase of ulcerative colitis. Inflammation was more severe in the transverse colon, with inflammation confined to the mucosa. There was only mild involvement of the ascending and sigmoid colon, and no significant involvement of the cecum, rectum, or terminal ileum. Family history included irritable bowel syndrome.
COLNTUN03	pINCY	This normalized pooled colon tumor tissue library was constructed from 1.16 million independent clones from a pooled colon tumor library. Starting library was constructed using pooled cDNA from 6 donors. cDNA was generated using mRNA isolated from colon tumor tissue removed from a 55-year-old Caucasian male (A) during hemicolectomy; from a 60-year-old Caucasian male (B) during hemicolectomy; from a 62-year-old Caucasian male (C) during sigmoidectomy; from a 30-year-old Caucasian female (D) during hemicolectomy; from a 64-year-old Caucasian female (E) during hemicolectomy; and from a 70-year-old Caucasian female (F) during hemicolectomy. Pathology indicated invasive grade 3 adenocarcinoma (A); invasive grade 2 adenocarcinoma (B); invasive grade 2 adenocarcinoma (C); carcinoid tumor (D); invasive grade 3 adenocarcinoma (E); and invasive grade 2 adenocarcinoma (F). Donors B, C, D, E, and F had positive lymph nodes. Patient medications included Ativan (A); Seldane (B), Tri-Levlen (D); Synthroid (E); Tamoxifen, prednisone, Synthroid, and Glipizide (F). The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.

Table 6 (cont.)

Library	Vector	Library Description
HEALDIR01	PCDNA2.1	This random primed library was constructed using RNA isolated from diseased left ventricle tissue removed from a 7-month-old Caucasian male who died from cardiopulmonary arrest due to Pompe's disease. Patient history included cleft lip, cleft palate, left ventricular hypertrophy, pyrexia, right complete cleft lip, congestive heart failure, chronic serous otitis media, hypertrophic cardiomyopathy, acute myocardial infarction, diabetes, cystic fibrosis and Down's syndrome.
LIVRNON08	pINCY	This normalized library was constructed from 5.7 million independent clones from a pooled liver tissue library. Starting RNA was made from pooled liver tissue removed from a 4-year-old Hispanic male who died from anoxia and a 16 week female fetus who died after 16-weeks gestation from anencephaly. Serologies were positive for cytomegalovirus in the 4-year-old. Patient history included asthma in the 4-year-old. Family history included taking daily prenatal vitamins and mitral valve prolapse in the mother of the fetus. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
LPARNOT02	pINCY	Library was constructed using RNA isolated from tissue obtained from the left parotid (salivary) gland of a 70-year-old male with parotid cancer.
LUNGNON07	pINCY	This normalized lung tissue library was constructed from 5.1 million independent clones from a lung tissue library. Starting RNA was made from RNA isolated from lung tissue. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 hours/round) reannealing hybridization was used.

Table 6 (cont.)

Library	Vector	Library Description
MIXDUNB01	pINCY	Library was constructed using RNA isolated from myometrium removed from a 41-year-old Caucasian female (A) during vaginal hysterectomy with a dilatation and curettage and untreated smooth muscle cells removed from the renal vein of a 57-year-old Caucasian male. Pathology for donor A indicated the myometrium and cervix were unremarkable. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Pathology for the associated tumor tissue indicated uterine leiomyoma. Medical history included an unspecified menstrual disorder, ventral hernia, normal delivery, a benign ovarian neoplasm, and tobacco abuse in donor A. Previous surgeries included a bilateral destruction of fallopian tubes, removal of a solitary ovary, and an exploratory laparotomy in donor A. Medications included ferrous sulfate in donor A.
OVARTUT05	pINCY	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 62-year-old Caucasian female during a total abdominal hysterectomy, removal of the fallopian tubes and ovaries, exploratory laparotomy, regional lymph node excision, and dilation and curettage. Pathology indicated a grade 4 endometrioid carcinoma with extensive squamous differentiation, forming a solid mass in the right ovary. The uterine endometrium was inactive, the cervix showed mild chronic cervicitis, and focal endometriosis was observed in the posterior uterine serosa. Curettings indicated weakly proliferative endometrium with excessive stromal breakdown in the uterus, and a prior cervical biopsy indicated mild chronic cervicitis with a prominent nabothian cyst in the cervix. Patient history included longitudinal deficiency of the radioluna, osteoarthritis, thrombophlebitis, and abnormal blood chemistries. Family history included atherosclerotic coronary artery disease, pulmonary embolism, and cerebrovascular disease.
PENITUT01	pINCY	Library was constructed using RNA isolated from tumor tissue removed from the penis of a 64-year-old Caucasian male during penile amputation. Pathology indicated a fungating invasive grade 4 squamous cell carcinoma involving the inner wall of the foreskin and extending onto the glans penis. Patient history included benign neoplasm of the large bowel, atherosclerotic coronary artery disease, angina pectoris, gout, and obesity. Family history included malignant pharyngeal neoplasm, chronic lymphocytic leukemia, and chronic liver disease.

Table 6 (cont.)

Library	Vector	Library Description
PITUDIR01	PCDNA2.1	This random primed library was constructed using RNA isolated from pituitary gland tissue removed from a 70-year-old female who died from metastatic adenocarcinoma.
PLACNOT05	pINCY	Library was constructed using RNA isolated from placental tissue removed from a Caucasian male fetus, who died after 18 weeks' gestation from fetal demise.
PROSTME06	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from diseased prostate tissue removed from a 57-year-old Caucasian male during closed prostatic biopsy, radical prostatectomy, and regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the matched tumor tissue indicated adenocarcinoma, Gleason grade 3+3, forming a predominant mass involving the right side centrally. The patient presented with elevated prostate specific antigen and prostate cancer. Patient history included tobacco abuse in remission. Previous surgeries included cholecystectomy, repair of diaphragm hernia, and repair of vertebral fracture. Patient medications included Pepsid, Omnipen, and Eulexin. Family history included benign hypertension, cerebrovascular accident, atherosclerotic coronary artery disease, uterine cancer and type II diabetes in the mother; prostate cancer in the father; drug abuse, prostate cancer, and breast cancer in the sibling(s).
TESTNOT11	pINCY	Library was constructed using RNA isolated from testicular tissue removed from a 16-year-old Caucasian male who died from hanging. Patient history included drug use (tobacco, marijuana, and cocaine use), and medications included Lithium, Ritalin, and Paxil.

Table 6 (cont.)

Library	Vector	Library Description
THYMNOE02	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from thymus tissue removed from a 3-year-old Hispanic male during a thymectomy and closure of a patent ductus arteriosus. The patient presented with severe pulmonary stenosis and cyanosis. Patient history included a cardiac catheterization and echocardiogram. Previous surgeries included Blalock-Taussig shunt and pulmonary valvotomy. The patient was not taking any medications. Family history included benign hypertension, osteoarthritis, depressive disorder, and extrinsic asthma in the grandparent(s).
THYMNO04	PSPORT1	This normalized library was constructed from a thymus tissue library. Starting RNA was made from thymus tissue removed from a 3-year-old Caucasian male, who died from anoxia. Serologies were negative. The patient was not taking any medications. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48-hours/round) reannealing hybridization was used.
THYRTUT03	pINCY	Library was constructed using RNA isolated from benign thyroid tumor tissue removed from a 17-year-old Caucasian male during a thyroidectomy. Pathology indicated encapsulated follicular adenoma forming a circumscribed mass.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) <i>J. Mol. Biol.</i> 215:403-410; Altschul, S.F. et al. (1997) <i>Nucleic Acids Res.</i> 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) <i>Proc. Natl. Acad. Sci. USA</i> 85:2444-2448; Pearson, W.R. (1990) <i>Methods Enzymol.</i> 183:63-98; and Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity=95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) <i>Nucleic Acids Res.</i> 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) <i>Methods Enzymol.</i> 266:88-105; and Attwood, T.K. et al. (1997) <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) <i>J. Mol. Biol.</i> 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) <i>Nucleic Acids Res.</i> 26:320-322; Durbin, R. et al. (1998) <i>Our World View</i> , in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value=1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score>GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-30,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-30,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, and
10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30.
2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-
30.
- 15 3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
- 20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:31-60.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
- 25 7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
- 30 9. A method of producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

5 11. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:31-60,

10 c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a
15 polynucleotide of claim 11.

13. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides
20 comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

30 a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected
5 from the group consisting of SEQ ID NO:1-30.

18. A method for treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition of claim 16.

10

19. A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

15

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- 25
- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
 - b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

30

24. A method for treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim

1, the method comprising:

a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a
5 compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, the method comprising:

a) combining the polypeptide of claim 1 with at least one test compound under conditions
10 permissive for the activity of the polypeptide of claim 1,

b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound,
and

c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change
15 in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method
20 comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts
25 of the compound and in the absence of the compound.

28. A method of assessing toxicity of a test compound, the method comprising:

a) treating a biological sample containing nucleic acids with the test compound,

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at
30 least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof,

c) quantifying the amount of hybridization complex, and

d) comparing the amount of hybridization complex in the treated biological sample with the
35

amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

5 29. A diagnostic test for a condition or disease associated with the expression of TRICH in a biological sample, the method comprising:

- a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex, and
 - b) detecting the complex, wherein the presence of the complex correlates with the presence
- 10 of the polypeptide in the biological sample.

30. The antibody of claim 10, wherein the antibody is:

- a) a chimeric antibody,
- b) a single chain antibody,
- 15 c) a Fab fragment,
- d) a F(ab')₂ fragment, or
- e) a humanized antibody.

20 31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim 31.

25 33. A composition of claim 31, wherein the antibody is labeled.

34. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim 33.

30 35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10, the method comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, or an immunogenic fragment thereof, under conditions to

elicit an antibody response,

- b) isolating antibodies from said animal, and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30.

36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

10

38. A method of making a monoclonal antibody with the specificity of the antibody of claim 10, the method comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- b) isolating antibody producing cells from the animal,
- c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells,
- d) culturing the hybridoma cells, and
- e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30.

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

43. A method of detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30 in a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide, and

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30 in the sample.

44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30 from a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide, and

b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-30.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.
64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.
65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.
66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.
67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.
68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.
69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.
70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.
71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:27.
72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.

73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.

74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.

5 75. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:31.

76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:32.

10 77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:33.

15 78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.

79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:35.

20 80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.

81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.

25 82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.

83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.

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84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.

85. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
5 NO:42.

87. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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10 88. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:44.

89. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:45.
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90. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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91. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
20 NO:47.

92. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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25 93. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:49.

94. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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95. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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NO:52.

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NO:53.

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98. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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99. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
10 NO:55.

100. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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15 101. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:57.

102. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:58.

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103. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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<110> INCYTE GENOMICS, INC.
YUE, Henry
THORNTON, Michael
RAMKUMAR, Jayalaxmi
TANG, Y. Tom
AZIMZAI, Yalda
BAUGHN, Mariah R.
YANG, Junming
YAO, Monique G.
LAL, Preeti
WALIA, Narinder K.
GANDHI, Ameena R.
HAFALIA, April J.A.
NGUYEN, Danniel B.
PATTERSON, Chandra
ELLIOTT, Vicki S.
TRIBOULEY, Catherine M.
LU, Dyung Aina M.
XU, Yuming
REDDY, Roopa
HERNANDEZ, Roberto
BOROWSKY, Mark L.
LO, Terence P.
LU, Yan
POLICKY, Jennifer L.
GREENE, Barrie D.
SANJANWALA, Madhu S.
RAUMANN, Brigitte E.
BURFORD, Neil
ISON, Craig H.
LEE, Ernestine A.
DING, Li
DAS, Debopriya
KALLICK, Deborah A.
KHAN, Farrah A.
SEILHAMER, Jeffrey J.

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60/231,434

<151> 2000-08-03; 2000-08-10; 2000-08-18; 2000-08-25; 2000-08-31;
2000-09-08

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Phe Val Pro Tyr Val	His Leu Ala Pro His	Ala Leu Asp Arg	Gly
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Gly Asp Ala Gly Ala	Arg Leu Val Cys Gly	Trp Leu Ala Asp	Gln
185	190	195	
Gly Trp Val Pro Leu	Pro Arg Leu Leu Ala	Val Phe Gly Ala	Leu
200	205	210	
Thr Gly Leu Gly Leu	Trp Val Val Gly Leu	Val Pro Val Val	Gly
215	220	225	
Gly Glu Glu Ser Trp	Gly Gly Pro Leu Leu	Ala Ala Ala Val	Ala
230	235	240	
Tyr Gly Leu Ser Ala	Gly Ser Tyr Ala Pro	Leu Val Phe Gly	Val
245	250	255	
Leu Pro Gly Leu Val	Gly Val Gly Gly Val	Val Gln Ala Thr	Gly
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Leu Val Met Met Leu	Met Ser Leu Gly Gly	Leu Leu Gly Pro	Pro
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Cys Ile Ile Phe Phe	Phe Val Val Pro Ile	Val Phe Leu Thr	Ile
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Phe Ser Phe Trp Trp	Leu Ser Tyr Trp Leu	Glu Gln Gly Ser	Gly
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Thr Asn Ser Ser Arg	Glu Ser Asn Gly Thr	Met Ala Asp Leu	Gly
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Asn Ile Ala Asp Asn	Pro Gln Leu Ser Phe	Tyr Gln Leu Val	Tyr

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	95	100	105		
Gly Ile Phe Thr	Lys Val Thr Arg Lys	Ala Ser Thr Ala Leu	His		
	110	115	120		
Asn Lys Leu Phe	Asn Lys Val Phe Arg	Cys Pro Met Ser Phe	Phe		
	125	130	135		
Asp Thr Ile Pro	Ile Gly Arg Leu Leu	Asn Cys Phe Ala Gly	Asp		
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Leu Glu Gln Leu	Asp Gln Leu Leu Pro	Ile Phe Ser Glu Gln	Phe		
	155	160	165		
Leu Val Leu Ser	Leu Met Val Ile Ala	Val Leu Leu Ile Val	Ser		
	170	175	180		
Val Leu Ser Pro	Tyr Ile Leu Leu Met	Gly Ala Ile Ile Met	Val		
	185	190	195		
Ile Cys Phe Ile	Tyr Tyr Met Met Phe	Lys Lys Ala Ile Gly	Val		
	200	205	210		
Phe Lys Arg Leu	Glu Asn Tyr Ser Arg	Ser Pro Leu Phe Ser	His		
	215	220	225		
Ile Leu Asn Ser	Leu Gln Gly Leu Ser	Ser Ile His Val Tyr	Gly		
	230	235	240		
Lys Thr Glu Asp	Phe Ile Ser Gln Phe	Lys Arg Leu Thr Asp	Ala		
	245	250	255		
Gln Asn Asn Tyr	Leu Leu Leu Phe Leu	Ser Ser Thr Arg Trp	Met		
	260	265	270		
Ala Leu Arg Leu	Glu Ile Met Thr Asn	Leu Val Thr Leu Ala	Val		
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Lys Val Met Ala	Val Asn Ile Val Leu	Gln Leu Ala Ser Ser	Phe		
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Gln His Gly Glu	Ile Ile Phe Gln Asp	Tyr His Met Lys Tyr	Arg		
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Gly His Glu Val	Val Gly Ile Val Gly	Arg Thr Gly Ser Gly	Lys		
	395	400	405		
Ser Ser Leu Gly	Met Ala Leu Phe Arg	Leu Val Glu Pro Met	Ala		
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Gly Arg Ile Leu	Ile Asp Gly Val Asp	Ile Cys Ser Ile Gly	Leu		
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Glu Asp Leu Arg	Ser Lys Leu Ser Val	Ile Pro Gln Asp Pro	Val		
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His Thr Asp Gln	Gln Ile Trp Asp Ala	Leu Glu Arg Thr Phe	Leu		
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Thr Lys Ala Ile	Ser Lys Phe Pro Lys	Lys Leu His Thr Asp	Val		
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Val Glu Asn Gly	Gly Tyr Phe Ser Val	Gly Glu Arg Gln Leu	Leu		
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Cys Ile Ala Arg	Ala Val Leu Arg Asn	Ser Lys Ile Ile Leu	Ile		
	515	520	525		
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Gln Arg Thr Ile	Arg Glu Ala Phe Gln	Gly Cys Thr Val Leu	Val		
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          35          40          45
Leu Ile Leu Ile Ser Met Met His Pro Asn Lys Lys Tyr Glu Glu
          50          55          60
Val Pro Asn Ile Glu Leu Asn Pro Met Asp Lys Phe Thr Leu Ser
          65          70          75
Asn Leu Ile Leu Gly Tyr Thr Pro Val Thr Asn Ile Thr Ser Ser
          80          85          90
Ile Met Gln Lys Val Ser Thr Asp His Leu Pro Asp Val Ile Ile
          95          100          105
Thr Glu Glu Tyr Thr Asn Glu Lys Glu Met Leu Thr Ser Ser Leu
          110          115          120
Ser Lys Pro Ser Asn Phe Val Gly Val Val Phe Lys Asp Ser Met
          125          130          135
Ser Tyr Glu Leu Arg Phe Phe Pro Asp Met Ile Pro Val Ser Ser
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          155          160          165
Ala Gln Tyr Trp Ser Ser Gly Phe Thr Val Leu Gln Ala Ser Ile
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Asp Ala Ala Ile Ile Gln Leu Lys Thr Asn Val Ser Leu Trp Lys
          185          190          195
Glu Leu Glu Ser Thr Lys Ala Val Ile Met Gly Glu Thr Ala Val
          200          205          210
Val Glu Ile Asp Thr Phe Pro Arg Gly Val Ile Leu Ile Tyr Leu
          215          220          225
Val Ile Ala Phe Ser Pro Phe Gly Tyr Phe Leu Ala Ile His Ile
          230          235          240
Val Ala Glu Lys Glu Lys Lys Ile Lys Glu Phe Leu Lys Ile Met
          245          250          255
Gly Leu His Asp Thr Ala Phe Trp Leu Ser Trp Val Leu Leu Tyr
          260          265          270
Thr Ser Leu Ile Phe Leu Met Ser Leu Leu Met Ala Val Ile Ala
          275          280          285
Thr Ala Ser Leu Leu Phe Pro Gln Ser Ser Ser Ile Val Ile Phe
          290          295          300
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Met Leu Thr Pro Leu Phe Lys Lys Ser Lys His Val Gly Ile Val
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His Leu Glu Asp Phe Asn Glu Gly Ala Ser Phe Ser Asn Leu Thr	380	385	390
Ala Gly Pro Tyr Pro Leu Ile Ile Thr Ile Ile Met Leu Thr Leu	395	400	405
Asn Ser Ile Phe Tyr Val Leu Leu Ala Val Tyr Leu Asp Gln Val	410	415	420
Ile Pro Gly Glu Phe Gly Leu Arg Arg Ser Ser Leu Tyr Phe Leu	425	430	435
Lys Pro Ser Tyr Trp Ser Lys Ser Lys Arg Asn Tyr Glu Glu Leu	440	445	450
Ser Glu Gly Asn Val Asn Gly Asn Ile Ser Phe Ser Glu Ile Ile	455	460	465
Glu Pro Val Ser Ser Glu Phe Val Gly Lys Glu Ala Ile Arg Ile	470	475	480
Ser Gly Ile Gln Lys Thr Tyr Arg Lys Lys Gly Glu Asn Val Glu	485	490	495
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Ala Leu Leu Gly His Ser Gly Thr Gly Lys Ser Thr Leu Met Asn	515	520	525
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Lys Met Ile Gly Ile Cys Pro Gln Leu Asp Ile His Phe Asp Val	560	565	570
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Asp Pro Cys Ser Arg His Ile Val Trp Asn Leu Leu Lys Tyr Arg	650	655	660
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Glu Ser Leu Ser Ser Leu Val Lys Gln His Ile Pro Gly Ala Thr	725	730	735
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His Ser Asn Leu Gly Val Ile Ser Tyr Gly Val Ser Met Thr Thr	770	775	780
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Pro	Ala	Ala	Ala	Gly	Glu	Glu	Ala	Trp	Arg	Arg	Gly	Arg	Ala	Ala	
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Pro	Ser	Arg	Asp	Asp	Gln	Arg	Leu	Arg	Pro	Met	Ala	Pro	Gly	Leu	
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Ser	Glu	Ala	Gly	Lys	Leu	Leu	Gly	Leu	Glu	Tyr	Pro	Glu	Arg	Gln	
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Arg	Leu	Ala	Ala	Ala	Val	Gly	Phe	Leu	Thr	Met	Ser	Gly	Val	Ile	
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Ser	Met	Ser	Ala	Pro	Phe	Phe	Leu	Gly	Lys	Ile	Ile	Asp	Ala	Ile	
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Tyr	Thr	Asn	Pro	Thr	Val	Asp	Tyr	Ser	Asp	Asn	Leu	Thr	Arg	Leu	
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Cys	Leu	Gly	Leu	Ser	Ala	Val	Phe	Leu	Cys	Gly	Ala	Ala	Ala	Asn	
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Ala	Ile	Arg	Val	Tyr	Leu	Met	Gln	Thr	Ser	Gly	Gln	Arg	Ile	Val	
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Asn	Arg	Leu	Arg	Thr	Ser	Leu	Phe	Ser	Ser	Ile	Leu	Arg	Gln	Glu	
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Val	Ala	Phe	Phe	Asp	Lys	Thr	Arg	Thr	Gly	Glu	Leu	Ile	Asn	Arg	
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Leu	Ser	Ser	Asp	Thr	Ala	Leu	Leu	Gly	Arg	Ser	Val	Thr	Glu	Asn	
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Leu	Ser	Asp	Gly	Leu	Arg	Ala	Gly	Ala	Gln	Ala	Ser	Val	Gly	Ile	
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Ser	Val	Val	Pro	Pro	Val	Ser	Ile	Ile	Ala	Val	Ile	Tyr	Gly	Arg	
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Tyr	Leu	Arg	Lys	Leu	Thr	Lys	Val	Thr	Gln	Asp	Ser	Leu	Ala	Gln	
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Ala	Thr	Gln	Leu	Ala	Glu	Glu	Arg	Ile	Gly	Asn	Val	Arg	Thr	Val	
				275					280					285	
Arg	Ala	Phe	Gly	Lys	Glu	Met	Thr	Glu	Ile	Glu	Lys	Tyr	Ala	Ser	
				290					295					300	
Lys	Val	Asp	His	Val	Met	Gln	Leu	Ala	Arg	Lys	Glu	Ala	Phe	Ala	
				305					310					315	
Arg	Ala	Gly	Phe	Phe	Gly	Ala	Thr	Gly	Leu	Ser	Gly	Asn	Leu	Ile	
				320					325					330	
Val	Leu	Ser	Val	Leu	Tyr	Lys	Gly	Gly	Leu	Leu	Met	Gly	Ser	Ala	
				335					340					345	
His	Met	Thr	Val	Gly	Glu	Leu	Ser	Ser	Phe	Leu	Met	Tyr	Ala	Phe	
				350					355					360	
Trp	Val	Gly	Ile	Ser	Ile	Gly	Gly	Leu	Ser	Ser	Phe	Tyr	Ser	Glu	
				365					370					375	
Leu	Met	Lys	Gly	Leu	Gly	Ala	Gly	Gly	Arg	Leu	Trp	Glu	Leu	Leu	
				380					385					390	
Glu	Arg	Glu	Pro	Lys	Leu	Pro	Phe	Asn	Glu	Gly	Val	Ile	Leu	Asn	
				395					400					405	
Glu	Lys	Ser	Phe	Gln	Gly	Ala	Leu	Glu	Phe	Lys	Asn	Val	His	Phe	
				410					415					420	
Ala	Tyr	Pro	Ala	Arg	Pro	Glu	Val	Pro	Ile	Phe	Gln	Asp	Phe	Ser	
				425					430					435	
Leu	Ser	Ile	Pro	Ser	Gly	Ser	Val	Thr	Ala	Leu	Val	Gly	Pro	Ser	
				440					445					450	
Gly	Ser	Gly	Lys	Ser	Thr	Val	Leu	Ser	Leu	Leu	Leu	Arg	Leu	Tyr	
				455					460					465	
Asp	Pro	Ala	Ser	Gly	Thr	Ile	Ser	Leu	Asp	Gly	His	Asp	Ile	Arg	
				470					475					480	
Gln	Leu	Asn	Pro	Val	Trp	Leu	Arg	Ser	Lys	Ile	Gly	Thr	Val	Ser	

	485	490	495
Gln Glu Pro Ile	Leu Phe Ser Cys Ser	Ile Ala Glu Asn Ile	Ala
	500	505	510
Tyr Gly Ala Asp	Asp Pro Ser Ser Val	Thr Ala Glu Glu Ile	Gln
	515	520	525
Arg Val Ala Glu	Val Ala Asn Thr Val	Ala Phe Ile Arg Asn	Phe
	530	535	540
Pro Gln Gly Phe	Asn Thr Val Val Gly	Glu Lys Gly Val Leu	Leu
	545	550	555
Ser Gly Gly Gln	Lys Gln Arg Ile Ala	Ile Ala Arg Ala Leu	Leu
	560	565	570
Lys Asn Pro Lys	Ile Leu Leu Leu Asp	Glu Ala Thr Ser Ala	Leu
	575	580	585
Asp Ala Glu Asn	Glu Tyr Leu Val Gln	Glu Ala Leu Asp Arg	Leu
	590	595	600
Met Asp Gly Arg	Thr Val Leu Val Ile	Ala His Arg Leu Ser	Thr
	605	610	615
Ile Lys Asn Ala	Asn Met Val Ala Val	Leu Asp Gln Gly Lys	Ile
	620	625	630
Thr Glu Tyr Gly	Lys His Glu Glu Leu	Leu Ser Lys Pro Asn	Gly
	635	640	645
Ile Tyr Arg Lys	Leu Met Asn Lys Gln	Ser Phe Ile Ser Ala	
	650	655	

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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3200979CD1

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Leu Tyr Lys Asn Phe Leu Lys Lys Trp Arg Ile Lys Arg Glu Phe	
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Ile Gly Leu Tyr Leu Cys Ile Phe Ser Glu His Phe Arg Ala Thr	
	35 40 45
Arg Phe Pro Glu Gln Pro Pro Lys Val Leu Gly Ser Val Asp Gln	
	50 55 60
Phe Asn Asp Ser Gly Leu Val Val Ala Tyr Thr Pro Val Ser Asn	
	65 70 75
Ile Thr Gln Arg Ile Met Asn Lys Met Ala Leu Ala Ser Phe Met	
	80 85 90
Lys Gly Arg Thr Val Ile Gly Thr Pro Asp Glu Glu Thr Met Asp	
	95 100 105
Ile Glu Leu Pro Lys Lys Tyr His Glu Met Val Gly Val Ile Phe	
	110 115 120
Ser Asp Thr Phe Ser Tyr Arg Leu Lys Phe Asn Trp Gly Tyr Arg	
	125 130 135
Ile Pro Val Ile Lys Glu His Ser Glu Tyr Thr Glu His Cys Trp	
	140 145 150
Ala Met His Gly Glu Ile Phe Cys Tyr Leu Ala Lys Tyr Trp Leu	
	155 160 165
Lys Gly Phe Val Ala Phe Gln Ala Ala Ile Asn Ala Ala Ile Ile	
	170 175 180
Glu Val Thr Thr Asn His Ser Val Met Glu Glu Leu Thr Ser Val	
	185 190 195
Ile Gly Ile Asn Met Lys Ile Pro Pro Phe Ile Ser Lys Gly Glu	
	200 205 210
Ile Met Asn Glu Trp Phe His Phe Thr Cys Leu Val Ser Phe Ser	

	215		220		225
Ser Phe Ile Tyr	Phe Ala Ser Leu Asn	Val Ala Arg Glu Arg	Gly		
	230		235		240
Lys Phe Lys Lys	Leu Met Thr Val Met	Gly Leu Arg Glu Ser	Ala		
	245		250		255
Phe Trp Leu Ser	Trp Gly Leu Thr Tyr	Ile Cys Phe Ile Phe	Ile		
	260		265		270
Met Ser Ile Phe	Met Ala Leu Val Ile	Thr Ser Ile Pro Ile	Val		
	275		280		285
Phe His Thr Gly	Phe Met Val Ile Phe	Thr Leu Tyr Ser Leu	Tyr		
	290		295		300
Gly Leu Ser Leu	Ile Ala Leu Ala Phe	Leu Met Ser Val Leu	Ile		
	305		310		315
Arg Lys Pro Met	Leu Ala Gly Leu Ala	Gly Phe Leu Phe Thr	Val		
	320		325		330
Phe Trp Gly Cys	Leu Gly Phe Thr Val	Leu Tyr Arg Gln Leu	Pro		
	335		340		345
Leu Ser Leu Gly	Trp Val Leu Ser Leu	Leu Ser Pro Phe Ala	Phe		
	350		355		360
Thr Ala Gly Met	Ala Gln Ile Thr His	Leu Asp Asn Tyr Leu	Ser		
	365		370		375
Gly Val Ile Phe	Pro Asp Pro Ser Gly	Asp Ser Tyr Lys Met	Ile		
	380		385		390
Ala Thr Phe Phe	Ile Leu Ala Phe Asp	Thr Leu Phe Tyr Leu	Ile		
	395		400		405
Phe Thr Leu Tyr	Phe Glu Arg Val Leu	Pro Asp Lys Asp Gly	His		
	410		415		420
Gly Asp Ser Pro	Leu Phe Phe Leu Lys	Ser Ser Phe Trp Ser	Lys		
	425		430		435
His Gln Asn Thr	His His Glu Ile Phe	Glu Asn Glu Ile Asn	Pro		
	440		445		450
Glu His Ser Ser	Asp Asp Ser Phe Glu	Pro Val Ser Pro Glu	Phe		
	455		460		465
His Gly Lys Glu	Ala Ile Arg Ile Arg	Asn Val Ile Lys Glu	Tyr		
	470		475		480
Asn Gly Lys Thr	Gly Lys Val Glu Ala	Leu Gln Gly Ile Phe	Phe		
	485		490		495
Asp Ile Tyr Glu	Gly Gln Ile Thr Ala	Ile Leu Gly His Asn	Gly		
	500		505		510
Ala Gly Lys Ser	Thr Leu Leu Asn Ile	Leu Ser Gly Leu Ser	Val		
	515		520		525
Ser Thr Glu Gly	Ser Ala Thr Ile Tyr	Asn Thr Gln Leu Ser	Glu		
	530		535		540
Ile Thr Asp Met	Glu Glu Ile Arg Lys	Asn Ile Gly Phe Cys	Pro		
	545		550		555
Gln Phe Asn Phe	Gln Phe Asp Phe Leu	Thr Val Arg Glu Asn	Leu		
	560		565		570
Arg Val Phe Ala	Lys Ile Lys Gly Ile	Gln Pro Lys Glu Val	Glu		
	575		580		585
Gln Glu Val Leu	Leu Leu Asp Glu Pro	Thr Ala Gly Leu Asp	Pro		
	590		595		600
Phe Ser Arg His	Arg Val Trp Ser Leu	Leu Lys Glu His Lys	Val		
	605		610		615
Asp Arg Leu Ile	Leu Phe Ser Thr Gln	Phe Met Asp Glu Ala	Asp		
	620		625		630
Ile Leu Ala Asp	Arg Lys Val Phe Leu	Ser Asn Gly Lys Leu	Lys		
	635		640		645
Cys Ala Gly Ser	Ser Leu Phe Leu Lys	Arg Lys Trp Gly Ile	Gly		
	650		655		660
Tyr His Leu Ser	Leu His Arg Asn Glu	Met Cys Asp Thr Glu	Lys		
	665		670		675
Ile Thr Ser Leu	Ile Lys Gln His Ile	Pro Asp Ala Lys Leu	Thr		
	680		685		690

Thr	Glu	Ser	Glu	Glu	Lys	Leu	Val	Tyr	Ser	Leu	Pro	Leu	Glu	Lys	
				695					700					705	
Thr	Asn	Lys	Phe	Pro	Asp	Leu	Tyr	Ser	Asp	Leu	Asp	Lys	Cys	Ser	
				710					715					720	
Asp	Gln	Gly	Ile	Arg	Asn	Tyr	Ala	Val	Ser	Val	Thr	Ser	Leu	Asn	
				725					730					735	
Glu	Val	Phe	Leu	Asn	Leu	Glu	Gly	Lys	Ser	Ala	Ile	Asp	Glu	Pro	
				740					745					750	
Asp	Phe	Asp	Ile	Gly	Lys	Gln	Glu	Lys	Ile	His	Val	Thr	Arg	Asn	
				755					760					765	
Thr	Gly	Asp	Glu	Ser	Glu	Met	Glu	Gln	Val	Leu	Cys	Ser	Leu	Pro	
				770					775					780	
Glu	Thr	Arg	Lys	Ala	Val	Ser	Ser	Ala	Ala	Leu	Trp	Arg	Arg	Gln	
				785					790					795	
Ile	Tyr	Ala	Val	Ala	Thr	Leu	Arg	Phe	Leu	Lys	Leu	Arg	Arg	Glu	
				800					805					810	
Arg	Arg	Ala	Leu	Leu	Cys	Leu	Leu	Leu	Val	Leu	Gly	Ile	Ala	Phe	
				815					820					825	
Ile	Pro	Ile	Ile	Leu	Glu	Lys	Ile	Met	Tyr	Lys	Val	Thr	Arg	Glu	
				830					835					840	
Thr	His	Cys	Trp	Glu	Phe	Ser	Pro	Ser	Met	Tyr	Phe	Leu	Ser	Leu	
				845					850					855	
Glu	Gln	Ile	Pro	Lys	Thr	Pro	Leu	Thr	Ser	Leu	Leu	Ile	Val	Asn	
				860					865					870	
Asn	Thr	Gly	Ser	Asn	Ile	Glu	Asp	Leu	Val	His	Ser	Leu	Lys	Cys	
				875					880					885	
Gln	Asp	Ile	Val	Leu	Glu	Ile	Asp	Asp	Phe	Arg	Asn	Arg	Asn	Gly	
				890					895					900	
Ser	Asp	Asp	Pro	Ser	Tyr	Asn	Gly	Ala	Ile	Ile	Val	Ser	Gly	Asp	
				905					910					915	
Gln	Lys	Asp	Tyr	Arg	Phe	Ser	Val	Ala	Cys	Asn	Thr	Lys	Lys	Ser	
				920					925					930	
Asn	Cys	Phe	Pro	Val	Leu	Met	Gly	Ile	Val	Ser	Asn	Ala	Leu	Ile	
				935					940					945	
Gly	Ile	Phe	Asn	Phe	Thr	Glu	Leu	Ile	Gln	Met	Glu	Ser	Thr	Ser	
				950					955					960	
Phe	Phe	Arg	Asp	Asp	Ile	Val	Leu	Asp	Leu	Gly	Phe	Ile	Asp	Gly	
				965					970					975	
Ser	Ile	Phe	Leu	Leu	Leu	Ile	Thr	Asn	Cys	Ile	Ser	Pro	Tyr	Ile	
				980					985					990	
Gly	Ile	Ser	Ser	Ile	Ser	Asp	Tyr	Lys	Ile	Pro	Ser	Ser	Ile	Pro	
				995					1000					1005	
Ser	Ile	Leu	Cys	Gln	Lys	Asn	Val	Gln	Ser	Gln	Leu	Trp	Ile	Ser	
				1010					1015					1020	
Gly	Leu	Trp	Pro	Ser	Ala	Tyr	Trp	Cys	Gly	Gln	Ala	Leu	Val	Asp	
				1025					1030					1035	
Ile	Pro	Leu	His	Phe	Leu	Ile	Leu	Leu	Ser	Ile	His	Leu	Ile	Tyr	
				1040					1045					1050	
Tyr	Phe	Ser	Phe	Leu	Gly	Phe	Gln	Leu	Pro	Trp	Glu	Leu	Met	Phe	
				1055					1060					1065	
Val	Leu	Val	Val	Cys	Ile	Ile	Gly	Cys	Ala	Ala	Ser	Leu	Ile	Phe	
				1070					1075					1080	
Leu	Met	Tyr	Val	Leu	Ser	Phe	Ile	Phe	Cys	Lys	Trp	Arg	Lys	Asn	
				1085					1090					1095	
Asn	Gly	Phe	Trp	Ser	Phe	Gly	Phe	Phe	Ile	Val	Leu	Ile	Cys	Val	
				1100					1105					1110	
Ser	Thr	Ile	Leu	Val	Ser	Thr	Lys	Tyr	Glu	Lys	Pro	Asn	Leu	Ile	
				1115					1120					1125	
Leu	Cys	Met	Ile	Phe	Ile	Pro	Ser	Phe	Thr	Phe	Leu	Asp	Met	Ser	
				1130					1135					1140	
Leu	Leu	Ile	Gln	Leu	Asn	Phe	Met	Tyr	Met	Arg	Asn	Leu	Asp	Ser	
				1145					1150					1155	
Leu	Asp	Asn	Arg	Ile	Asn	Glu	Val	Asn	Lys	Thr	Ile	Leu	Leu	Thr	

1160	1165	1170
Asn Leu Ile Pro Tyr Leu Gln Ser Val Ile Phe Leu Phe Val Ile		
1175	1180	1185
Arg Cys Leu Glu Met Lys Tyr Gly Asn Glu Ile Met Asn Lys Asp		
1190	1195	1200
Pro Val Phe Arg Ile Ser Pro Arg Ser Arg Gly Thr His Thr Asn		
1205	1210	1215
Pro Glu Glu Pro Glu Glu Asp Val Gln Ala Glu Arg Val Gln Ala		
1220	1225	1230
Ala Asn Ala Leu Thr Thr Pro Asn Leu Glu Glu Pro Val Ile		
1235	1240	1245
Thr Ala Ser Cys Leu His Lys Glu Tyr Tyr Glu Thr Lys Lys Ser		
1250	1255	1260
Cys Phe Ser Thr Thr Lys Lys Lys Ala Ala Ile Arg Asn Val Ser		
1265	1270	1275
Phe Cys Val Lys Lys Gly Glu Val Leu Gly Leu Leu Gly His Asn		
1280	1285	1290
Gly Ala Gly Lys Ser Thr Ser Ile Lys Met Ile Thr Gly Cys Thr		
1295	1300	1305
Val Pro Thr Ala Gly Val Val Val Leu Gln Gly Asn Arg Ala Ser		
1310	1315	1320
Val Arg Gln Gln Arg Asp Asn Ser Leu Lys Phe Leu Gly Tyr Cys		
1325	1330	1335
Pro Gln Glu Asn Ser Leu Trp Pro Lys Leu Thr Met Lys Glu His		
1340	1345	1350
Leu Glu Leu Tyr Ala Ala Val Lys Gly Leu Gly Lys Glu Asp Ala		
1355	1360	1365
Ala Leu Ser Ile Ser Arg Leu Val Glu Ala Leu Lys Leu Gln Glu		
1370	1375	1380
Gln Leu Lys Ala Pro Val Lys Thr Leu Ser Glu Gly Ile Lys Arg		
1385	1390	1395
Lys Leu Cys Phe Val Leu Ser Ile Leu Gly Asn Pro Ser Val Val		
1400	1405	1410
Leu Leu Asp Glu Pro Phe Thr Gly Met Asp Pro Glu Gly Gln Gln		
1415	1420	1425
Gln Met Trp Gln Ile Leu Gln Ala Thr Ile Lys Asn Gln Glu Arg		
1430	1435	1440
Gly Thr Leu Leu Thr Thr His Tyr Met Ser Glu Ala Lys Ser Leu		
1445	1450	1455
Cys Asp Arg Val Ala Ile Met Val Ser Gly Thr Leu Arg Cys Ile		
1460	1465	1470
Gly Ser Ile Gln His Leu Lys Asn Lys Phe Gly Lys Asp Tyr Leu		
1475	1480	1485
Leu Glu Ile Lys Met Lys Glu Pro Thr Gln Val Glu Ala Leu His		
1490	1495	1500
Thr Glu Ile Leu Lys Leu Phe Pro Gln Ala Ala Trp Gln Glu Arg		
1505	1510	1515
Tyr Ser Ser Leu Met Ala Tyr Lys Leu Pro Val Glu Asp Val His		
1520	1525	1530
Pro Leu Ser Arg Ala Phe Phe Lys Leu Glu Ala Met Lys Gln Thr		
1535	1540	1545
Phe Asn Leu Glu Glu Tyr Ser Leu Ser Gln Ala Thr Leu Glu Gln		
1550	1555	1560
Val Phe Leu Glu Leu Cys Lys Glu Gln Glu Leu Gly Asn Val Asp		
1565	1570	1575
Asp Lys Ile Asp Thr Thr Val Glu Trp Lys Leu Leu Pro Gln Glu		
1580	1585	1590
Asp Pro		

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<213> Homo sapiens

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Gly Gly Leu Asp Ala Ile Arg Ile Pro Ser Ser Leu Val Trp Arg
          35          40          45
Pro Asp Ile Val Leu Tyr Asn Lys Ala Asp Ala Gln Pro Pro Gly
          50          55          60
Ser Ala Ser Thr Asn Val Val Leu Arg His Asp Gly Ala Val Arg
          65          70          75
Trp Asp Ala Pro Ala Ile Thr Arg Ser Ser Cys Arg Val Asp Val
          80          85          90
Ala Ala Phe Pro Phe Asp Ala Gln His Cys Gly Leu Thr Phe Gly
          95          100          105
Ser Trp Thr His Gly Gly His Gln Val Asp Val Arg Pro Arg Gly
          110          115          120
Ala Ala Ala Ser Leu Ala Asp Phe Val Glu Asn Val Glu Trp Arg
          125          130          135
Val Leu Gly Met Pro Ala Arg Arg Arg Val Leu Thr Tyr Gly Cys
          140          145          150
Cys Ser Glu Pro Tyr Pro Asp Val Thr Phe Thr Leu Leu Leu Arg
          155          160          165
Arg Arg Ala Ala Ala Tyr Val Cys Asn Leu Leu Leu Pro Cys Val
          170          175          180
Leu Ile Ser Leu Leu Ala Pro Leu Ala Phe His Leu Pro Ala Asp
          185          190          195
Ser Gly Glu Lys Val Ser Leu Gly Val Thr Val Leu Leu Ala Leu
          200          205          210
Thr Val Phe Gln Leu Leu Leu Ala Glu Ser Met Pro Pro Ala Glu
          215          220          225
Ser Val Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr Met Thr Met
          230          235          240
Val Thr Phe Ser Thr Ala Leu Thr Ile Leu Ile Met Asn Leu His
          245          250          255
Tyr Cys Gly Pro Ser Val Arg Pro Val Pro Ala Trp Ala Arg Ala
          260          265          270
Leu Leu Leu Gly His Leu Ala Arg Gly Leu Cys Val Arg Glu Arg
          275          280          285
Gly Glu Pro Cys Gly Gln Ser Arg Pro Pro Glu Leu Ser Pro Ser
          290          295          300
Pro Gln Ser Pro Glu Gly Gly Ala Gly Pro Pro Ala Gly Pro Cys
          305          310          315
His Glu Pro Arg Cys Leu Cys Arg Gln Glu Ala Leu Leu His His
          320          325          330
Val Ala Thr Ile Ala Asn Thr Phe Arg Ser His Arg Ala Ala Gln
          335          340          345
Arg Cys His Glu Asp Trp Lys Arg Leu Ala Arg Val Met Asp Arg
          350          355          360
Phe Phe Leu Ala Ile Phe Phe Ser Met Ala Leu Val Met Ser Leu
          365          370          375
Leu Val Leu Val Gln Ala Leu
          380

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<211> 1115

<212> PRT

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<223> Incyte ID No: 6996659CD1

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20      25      30
Ser Ser Ser His Pro Gln Pro Cys Gln Ile Leu Lys Arg Ile Gly
35      40      45
His Ala Val Arg Val Gly Ala Val His Leu Gln Pro Trp Thr Thr
50      55      60
Ala Pro Arg Ala Ala Ser Arg Ala Pro Asp Asp Ser Arg Ala Gly
65      70      75
Ala Gln Arg Asp Glu Pro Glu Pro Gly Thr Arg Arg Ser Pro Ala
80      85      90
Pro Ser Pro Gly Ala Arg Trp Leu Gly Ser Thr Leu His Gly Arg
95      100      105
Gly Pro Pro Gly Ser Arg Lys Pro Gly Glu Gly Ala Arg Ala Glu
110      115      120
Ala Leu Trp Pro Arg Asp Ala Leu Leu Phe Ala Val Asp Asn Leu
125      130      135
Asn Arg Val Glu Gly Leu Leu Pro Tyr Asn Leu Ser Leu Glu Val
140      145      150
Val Met Ala Ile Glu Ala Gly Leu Gly Asp Leu Pro Leu Leu Pro
155      160      165
Phe Ser Ser Pro Ser Ser Pro Trp Ser Ser Asp Pro Phe Ser Phe
170      175      180
Leu Gln Ser Val Cys His Thr Val Val Val Gln Gly Val Ser Ala
185      190      195
Leu Leu Ala Phe Pro Gln Ser Gln Gly Glu Met Met Glu Leu Asp
200      205      210
Leu Val Ser Leu Val Leu His Ile Pro Val Ile Ser Ile Val Arg
215      220      225
His Glu Phe Pro Arg Glu Ser Gln Asn Pro Leu His Leu Gln Leu
230      235      240
Ser Leu Glu Asn Ser Leu Ser Ser Asp Ala Asp Val Thr Val Ser
245      250      255
Ile Leu Thr Met Asn Asn Trp Tyr Asn Phe Ser Leu Leu Leu Cys
260      265      270
Gln Glu Asp Trp Asn Ile Thr Asp Phe Leu Leu Leu Thr Gln Asn
275      280      285
Asn Ser Lys Phe His Leu Gly Ser Ile Ile Asn Ile Thr Ala Asn
290      295      300
Leu Pro Ser Thr Gln Asp Leu Leu Ser Phe Leu Gln Ile Gln Leu
305      310      315
Glu Ser Ile Lys Asn Ser Thr Pro Thr Val Val Met Phe Gly Cys
320      325      330
Asp Met Glu Ser Ile Arg Arg Ile Phe Glu Ile Thr Thr Gln Phe
335      340      345
Gly Val Met Pro Pro Glu Leu Arg Trp Val Leu Gly Asp Ser Gln
350      355      360
Asn Val Glu Glu Leu Arg Thr Glu Gly Leu Pro Leu Gly Leu Ile
365      370      375
Ala His Gly Lys Thr Thr Gln Ser Val Phe Glu His Tyr Val Gln
380      385      390
Asp Ala Met Glu Leu Val Ala Arg Ala Val Ala Thr Ala Thr Met
395      400      405
Ile Gln Pro Glu Leu Ala Leu Ile Pro Ser Thr Met Asn Cys Met
410      415      420

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Glu Val Glu Thr	Thr Asn Leu Thr Ser Gly Gln Tyr Leu Ser Arg	425	430	435
Phe Leu Ala Asn	Thr Thr Phe Arg Gly Leu Ser Gly Ser Ile Arg	440	445	450
Val Lys Gly Ser	Thr Ile Val Ser Ser Glu Asn Asn Phe Phe Ile	455	460	465
Trp Asn Leu Gln	His Asp Pro Met Gly Lys Pro Met Trp Thr Arg	470	475	480
Leu Gly Ser Trp	Gln Gly Gly Lys Ile Val Met Asp Tyr Gly Ile	485	490	495
Trp Pro Glu Gln	Ala Gln Arg His Lys Thr His Phe Gln His Pro	500	505	510
Ser Lys Leu His	Leu Arg Val Val Thr Leu Ile Glu His Pro Phe	515	520	525
Val Phe Thr Arg	Glu Val Asp Asp Glu Gly Leu Cys Pro Ala Gly	530	535	540
Gln Leu Cys Leu	Asp Pro Met Thr Asn Asp Ser Ser Thr Leu Asp	545	550	555
Ser Leu Phe Ser	Ser Leu His Ser Ser Asn Asp Thr Val Pro Ile	560	565	570
Lys Phe Lys Lys	Cys Cys Tyr Gly Tyr Cys Ile Asp Leu Leu Glu	575	580	585
Lys Ile Ala Glu	Asp Met Asn Phe Asp Phe Asp Leu Tyr Ile Val	590	595	600
Gly Asp Gly Lys	Tyr Gly Ala Trp Lys Asn Gly His Trp Thr Gly	605	610	615
Leu Val Gly Asp	Leu Leu Arg Gly Thr Ala His Met Ala Val Thr	620	625	630
Ser Phe Ser Ile	Asn Thr Ala Arg Ser Gln Val Ile Asp Phe Thr	635	640	645
Ser Pro Phe Phe	Ser Thr Ser Leu Gly Ile Leu Val Arg Thr Arg	650	655	660
Asp Thr Ala Ala	Pro Ile Gly Ala Phe Met Trp Pro Leu His Trp	665	670	675
Thr Met Trp Leu	Gly Ile Phe Val Ala Leu His Ile Thr Ala Val	680	685	690
Phe Leu Thr Leu	Tyr Glu Trp Lys Ser Pro Phe Gly Leu Thr Ser	695	700	705
Lys Gly Arg Asn	Arg Ser Lys Val Phe Ser Phe Ser Ser Ala Leu	710	715	720
Asn Ile Cys Tyr	Ala Leu Leu Phe Gly Arg Thr Val Ala Ile Lys	725	730	735
Pro Pro Lys Cys	Trp Thr Gly Arg Phe Leu Met Asn Leu Trp Ala	740	745	750
Ile Phe Cys Met	Phe Cys Leu Ser Thr Tyr Thr Ala Asn Leu Ala	755	760	765
Ala Val Met Val	Gly Glu Lys Ile Tyr Glu Glu Leu Ser Gly Ile	770	775	780
His Asp Pro Lys	Leu His His Pro Ser Gln Gly Phe Arg Phe Gly	785	790	795
Thr Val Arg Glu	Ser Ser Ala Glu Asp Tyr Val Arg Gln Ser Phe	800	805	810
Pro Glu Met His	Glu Tyr Met Arg Arg Tyr Asn Val Pro Ala Thr	815	820	825
Pro Asp Gly Val	Glu Tyr Leu Lys Asn Asp Pro Glu Lys Leu Asp	830	835	840
Ala Phe Ile Met	Asp Lys Ala Leu Leu Asp Tyr Glu Val Ser Ile	845	850	855
Asp Ala Asp Cys	Lys Leu Leu Thr Val Gly Lys Pro Phe Ala Ile	860	865	870
Glu Gly Tyr Gly	Ile Gly Leu Pro Pro Asn Ser Pro Leu Thr Ala	875	880	885
Asn Ile Ser Glu	Leu Ile Ser Gln Tyr Lys Ser His Gly Phe Met			

	890	895	900
Asp Met Leu His	Asp Lys Trp Tyr Arg	Val Val Pro Cys Gly Lys	
	905	910	915
Arg Ser Phe Ala	Val Thr Glu Thr Leu	Gln Met Gly Ile Lys His	
	920	925	930
Phe Ser Gly Leu	Phe Val Leu Leu Cys	Ile Gly Phe Gly Leu Ser	
	935	940	945
Ile Leu Thr Thr	Ile Gly Glu His Ile	Val Tyr Arg Leu Leu Leu	
	950	955	960
Pro Arg Ile Lys	Asn Lys Ser Lys Leu	Gln Tyr Trp Leu His Thr	
	965	970	975
Ser Gln Arg Leu	His Arg Ala Ile Asn	Thr Ser Phe Ile Glu Glu	
	980	985	990
Lys Gln Gln His	Phe Lys Thr Lys Arg	Val Glu Lys Arg Ser Asn	
	995	1000	1005
Val Gly Pro Arg	Gln Leu Thr Val Trp	Asn Thr Ser Asn Leu Ser	
	1010	1015	1020
His Asp Asn Arg	Arg Lys Tyr Ile Phe	Ser Asp Glu Glu Gly Gln	
	1025	1030	1035
Asn Gln Leu Gly	Ile Arg Ile His Gln	Asp Ile Pro Leu Pro Pro	
	1040	1045	1050
Arg Arg Arg Glu	Leu Pro Ala Leu Arg	Thr Thr Asn Gly Lys Ala	
	1055	1060	1065
Asp Ser Leu Asn	Val Ser Arg Asn Ser	Val Met Gln Glu Leu Ser	
	1070	1075	1080
Glu Leu Glu Lys	Gln Ile Gln Val Ile	Arg Gln Glu Leu Gln Leu	
	1085	1090	1095
Ala Val Ser Arg	Lys Thr Glu Leu Glu	Glu Tyr Gln Arg Thr Ser	
	1100	1105	1110
Arg Thr Cys Glu	Ser		
	1115		

<210> 8

<211> 295

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472747CD1

<400> 8

Met Pro Ser Ala	Gly Leu Cys Ser Cys Trp	Gly Gly Arg Val Leu	
1	5	10	15
Pro Leu Leu Leu	Ala Tyr Val Cys Tyr	Leu Leu Gly Ala Thr	
	20	25	30
Ile Phe Gln Leu	Leu Glu Arg Gln Ala	Glu Ala Gln Ser Arg Asp	
	35	40	45
Gln Phe Gln Leu	Glu Lys Leu Arg Phe	Leu Glu Asn Tyr Thr Cys	
	50	55	60
Leu Asp Gln Trp	Ala Met Glu Gln Phe	Val Gln Val Ile Met Glu	
	65	70	75
Ala Trp Val Lys	Gly Val Asn Pro Lys	Gly Asn Ser Thr Asn Pro	
	80	85	90
Ser Asn Trp Asp	Phe Gly Ser Ser Phe	Phe Phe Ala Gly Thr Val	
	95	100	105
Val Thr Thr Ile	Gly Tyr Gly Asn Leu	Ala Pro Ser Thr Glu Ala	
	110	115	120
Gly Gln Val Phe	Cys Val Phe Tyr Ala	Leu Leu Gly Ile Pro Leu	
	125	130	135
Asn Val Ile Phe	Leu Asn His Leu Gly	Thr Gly Leu Arg Ala His	
	140	145	150
Leu Ala Ala Ile	Glu Arg Trp Glu Asp	Arg Pro Arg Arg Ser Gln	

	155		160		165
Glu Val Leu Gln	Val Leu Gly Leu Ala	Leu Phe Leu Thr Leu	Gly		
	170		175		180
Thr Leu Val Ile	Leu Ile Phe Pro Pro	Met Val Phe Ser His	Val		
	185		190		195
Glu Gly Trp Ser	Phe Ser Glu Gly Phe	Tyr Phe Ala Phe Ile	Thr		
	200		205		210
Leu Ser Thr Ile	Gly Phe Gly Asp Tyr	Val Ala Gly Thr Asp	Pro		
	215		220		225
Ser Lys His Tyr	Ile Ser Val Tyr Arg	Ser Leu Ala Ala Ile	Trp		
	230		235		240
Ile Leu Leu Gly	Leu Ala Trp Leu Ala	Leu Ile Leu Pro Leu	Gly		
	245		250		255
Pro Leu Leu Leu	His Arg Cys Cys Gln	Leu Trp Leu Leu Ser	Arg		
	260		265		270
Gly Leu Gly Val	Lys Asp Gly Ala Ala	Ser Asp Pro Ser Gly	Leu		
	275		280		285
Pro Arg Pro Gln	Lys Ile Pro Ile Ser	Ala			
	290		295		

<210> 9

<211> 384

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474121CD1

<400> 9

Met Glu Val Ser Gly	His Pro Gln Ala Arg	Arg Cys Cys Pro Glu
1	5	10
Ala Leu Gly Lys Leu	Phe Pro Gly Leu Cys	Phe Leu Cys Phe Leu
	20	25
Val Thr Tyr Ala Leu	Val Gly Ala Val Val	Phe Ser Ala Ile Glu
	35	40
Asp Gly Gln Val Leu	Val Ala Ala Asp Asp	Gly Glu Phe Glu Lys
	50	55
Phe Leu Glu Glu Leu	Cys Arg Ile Leu Asn	Cys Ser Glu Thr Val
	65	70
Val Glu Asp Arg Lys	Gln Asp Leu Gln Gly	His Leu Gln Lys Val
	80	85
Lys Pro Gln Trp Phe	Asn Arg Thr Thr His	Trp Ser Phe Leu Ser
	95	100
Ser Leu Phe Phe Cys	Cys Thr Val Phe Ser	Thr Val Gly Tyr Gly
	110	115
Tyr Ile Tyr Pro Val	Thr Arg Leu Gly Lys	Tyr Leu Cys Met Leu
	125	130
Tyr Ala Leu Phe Gly	Ile Pro Leu Met Phe	Leu Val Leu Thr Asp
	140	145
Thr Gly Asp Ile Leu	Ala Thr Ile Leu Ser	Thr Ser Tyr Asn Arg
	155	160
Phe Arg Lys Phe Pro	Phe Phe Thr Arg Pro	Leu Leu Ser Lys Trp
	170	175
Cys Pro Lys Ser Leu	Phe Lys Lys Lys Pro	Asp Pro Lys Pro Ala
	185	190
Asp Glu Ala Val Pro	Gln Ile Ile Ile Ser	Ala Glu Glu Leu Pro
	200	205
Gly Pro Lys Leu Gly	Thr Cys Pro Ser Arg	Pro Ser Cys Ser Met
	215	220
Glu Leu Phe Glu Arg	Ser His Ala Leu Glu	Lys Gln Asn Thr Leu
	230	235
Gln Leu Pro Pro Gln	Ala Met Glu Arg Ser	Asn Ser Cys Pro Glu

	245		250		255
Leu Val Leu Gly Arg	Leu Ser Tyr Ser	Ile Ile Ser Asn Leu Asp			
	260		265		270
Glu Val Gly Gln Gln	Val Glu Arg Leu Asp	Ile Pro Leu Pro Ile			
	275		280		285
Ile Ala Leu Ile Val	Phe Ala Tyr Ile	Ser Cys Ala Ala Ala Ile			
	290		295		300
Leu Pro Phe Trp Glu	Thr Gln Leu Asp	Phe Glu Asn Ala Phe Tyr			
	305		310		315
Phe Cys Phe Val Thr	Leu Thr Thr Ile	Gly Phe Gly Asp Thr Val			
	320		325		330
Leu Glu His Pro Asn	Phe Phe Leu Phe	Phe Ser Ile Tyr Ile Ile			
	335		340		345
Val Gly Met Glu Ile	Val Phe Ile Ala	Phe Lys Leu Val Gln Asn			
	350		355		360
Arg Leu Ile Asp Ile	Tyr Lys Asn Val	Met Leu Phe Phe Ala Lys			
	365		370		375
Gly Lys Phe Tyr His	Leu Val Lys Lys				
	380				

<210> 10

<211> 769

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475615CD1

<400> 10

Met Val Ser Pro Lys	Met Tyr Leu Ser Thr	Glu Ile Arg Asn Thr	
1	5	10	15
Phe Arg Leu Pro Ala	Pro Gln Thr His Leu	Gln Pro Cys Pro Ala	
	20	25	30
Gly Phe Ala His Pro	Leu Leu Val Asn Ala	Pro Asp Met Ser Gln	
	35	40	45
Pro Arg Pro Arg Tyr	Val Val Asp Arg Ala	Ala Tyr Ser Leu Thr	
	50	55	60
Leu Phe Asp Asp Glu	Phe Glu Lys Lys Asp	Arg Thr Tyr Pro Val	
	65	70	75
Gly Glu Lys Leu Arg	Asn Ala Phe Arg Cys	Ser Ser Ala Lys Ile	
	80	85	90
Lys Ala Val Val Phe	Gly Leu Leu Pro Val	Leu Ser Trp Leu Pro	
	95	100	105
Lys Tyr Lys Ile Lys	Asp Tyr Ile Ile Pro	Asp Leu Leu Gly Gly	
	110	115	120
Leu Ser Gly Gly Ser	Ile Gln Val Pro Gln	Gly Met Ala Phe Ala	
	125	130	135
Leu Leu Ala Asn Leu	Pro Ala Val Asn Gly	Leu Tyr Ser Ser Phe	
	140	145	150
Phe Pro Leu Leu Thr	Tyr Phe Phe Leu Gly	Gly Val His Gln Met	
	155	160	165
Val Pro Gly Thr Phe	Ala Val Ile Ser Ile	Leu Val Gly Asn Ile	
	170	175	180
Cys Leu Gln Leu Ala	Pro Glu Ser Lys Phe	Gln Val Phe Asn Asn	
	185	190	195
Ala Thr Asn Glu Ser	Tyr Val Asp Thr Ala	Ala Met Glu Ala Glu	
	200	205	210
Arg Leu His Val Ser	Ala Thr Leu Ala Cys	Leu Thr Ala Ile Ile	
	215	220	225
Gln Met Gly Leu Gly	Phe Met Gln Phe Gly	Phe Val Ala Ile Tyr	
	230	235	240
Leu Ser Glu Ser Phe	Ile Arg Gly Phe Met	Thr Ala Ala Gly Leu	

	245	250	255
Gln Ile Leu Ile Ser Val Leu Lys Tyr	Ile Phe Gly Leu Thr	Ile	
	260	265	270
Pro Ser Tyr Thr Gly Pro Gly Ser Ile	Val Phe Thr Phe Ile	Asp	
	275	280	285
Ile Cys Lys Asn Leu Pro His Thr Asn	Ile Ala Ser Leu Ile	Phe	
	290	295	300
Ala Leu Ile Ser Gly Ala Phe Leu Val	Leu Val Lys Glu Leu	Asn	
	305	310	315
Ala Arg Tyr Met His Lys Ile Arg Phe	Pro Ile Pro Thr Glu	Met	
	320	325	330
Ile Val Val Val Val Ala Thr Ala Ile	Ser Gly Gly Cys Lys	Met	
	335	340	345
Pro Lys Lys Tyr His Met Gln Ile Val	Gly Glu Ile Gln Arg	Gly	
	350	355	360
Phe Pro Thr Pro Val Ser Pro Val Val	Ser Gln Trp Lys Asp	Met	
	365	370	375
Ile Gly Thr Ala Phe Ser Leu Ala Ile	Val Ser Tyr Val Ile	Asn	
	380	385	390
Leu Ala Met Gly Arg Thr Leu Ala Asn	Lys His Gly Tyr Asp	Val	
	395	400	405
Asp Ser Asn Gln Glu Met Ile Ala Leu	Gly Cys Ser Asn Phe	Phe	
	410	415	420
Gly Ser Phe Phe Lys Ile His Val Ile	Cys Cys Ala Leu Ser	Val	
	425	430	435
Thr Leu Ala Val Asp Gly Ala Gly Gly	Lys Ser Gln Ser Val	Leu	
	440	445	450
Gly Ala Leu Ile Ala Val Asn Leu Lys	Asn Ser Leu Lys Gln	Leu	
	455	460	465
Thr Asp Pro Tyr Tyr Leu Trp Arg Lys	Ser Lys Leu Asp Cys	Cys	
	470	475	480
Ile Trp Val Val Ser Phe Leu Ser Ser	Phe Phe Leu Ser Leu	Pro	
	485	490	495
Tyr Gly Val Ala Val Gly Val Ala Phe	Ser Val Leu Val Val	Val	
	500	505	510
Phe Gln Thr Gln Phe Arg Asn Gly Tyr	Ala Leu Ala Gln Val	Met	
	515	520	525
Asp Thr Asp Ile Tyr Val Asn Pro Lys	Thr Tyr Asn Arg Ala	Gln	
	530	535	540
Asp Ile Gln Gly Ile Lys Ile Ile Thr	Tyr Cys Ser Pro Leu	Tyr	
	545	550	555
Phe Ala Asn Ser Glu Ile Phe Arg Gln	Lys Val Ile Ala Lys	Thr	
	560	565	570
Val Ser Leu Gln Glu Leu Gln Gln Asp	Phe Glu Asn Ala Pro	Pro	
	575	580	585
Thr Asp Pro Asn Asn Asn Gln Thr Pro	Ala Asn Gly Thr Ser	Val	
	590	595	600
Ser Tyr Ile Thr Phe Ser Pro Asp Ser	Ser Ser Pro Ala Gln	Ser	
	605	610	615
Glu Pro Pro Ala Ser Ala Glu Ala Pro	Gly Glu Pro Ser Asp	Met	
	620	625	630
Leu Ala Ser Val Pro Pro Phe Val Thr	Phe His Thr Leu Ile	Leu	
	635	640	645
Asp Met Ser Gly Val Ser Phe Val Asp	Leu Met Gly Ile Lys	Ala	
	650	655	660
Leu Ala Lys Leu Ser Ser Thr Tyr Gly	Lys Ile Gly Val Lys	Val	
	665	670	675
Phe Leu Val Asn Ile His Ala Gln Val	Tyr Asn Asp Ile Ser	His	
	680	685	690
Gly Gly Val Phe Glu Asp Gly Ser Leu	Glu Cys Lys His Val	Phe	
	695	700	705
Pro Ser Ile His Asp Ala Val Leu Phe	Ala Gln Ala Asn Ala	Arg	
	710	715	720

Asp Val Thr Pro Gly His Asn Phe Gln Gly Ala Pro Gly Asp Ala
 725 730 735
 Glu Leu Ser Leu Tyr Asp Ser Glu Glu Asp Ile Arg Ser Tyr Trp
 740 745 750
 Asp Leu Glu Gln Glu Met Phe Gly Ser Met Phe His Ala Glu Thr
 755 760 765
 Leu Thr Ala Leu

<210> 11
 <211> 882
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7475656CD1

<400> 11
 Met Glu Gly Gly Gly Lys Pro Asn Ser Ser Ser Asn Ser Arg Asp
 1 5 10 15
 Asp Gly Asn Ser Val Phe Pro Ala Lys Ala Ser Ala Pro Gly Ala
 20 25 30
 Gly Pro Ala Ala Ala Glu Lys Arg Leu Gly Thr Pro Pro Gly Gly
 35 40 45
 Gly Gly Ala Gly Ala Lys Glu His Gly Asn Ser Val Cys Phe Lys
 50 55 60
 Val Asp Gly Gly Gly Gly Glu Glu Pro Ala Gly Gly Phe Glu Asp
 65 70 75
 Ala Glu Gly Pro Arg Arg Gln Tyr Gly Phe Met Gln Arg Gln Phe
 80 85 90
 Thr Ser Met Leu Gln Pro Gly Val Asn Lys Phe Ser Leu Arg Met
 95 100 105
 Phe Gly Ser Gln Lys Ala Val Glu Lys Glu Gln Glu Arg Val Lys
 110 115 120
 Thr Ala Gly Phe Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe
 125 130 135
 Tyr Trp Asp Leu Ile Met Leu Ile Met Met Val Gly Asn Leu Val
 140 145 150
 Ile Ile Pro Val Gly Ile Thr Phe Phe Thr Glu Gln Thr Thr Thr
 155 160 165
 Pro Trp Ile Ile Phe Asn Val Ala Ser Asp Thr Val Phe Leu Leu
 170 175 180
 Asp Leu Ile Met Asn Phe Arg Thr Gly Thr Val Asn Glu Asp Ser
 185 190 195
 Ser Glu Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr Leu
 200 205 210
 Lys Ser Trp Phe Val Val Asp Phe Ile Ser Ser Ile Pro Val Asp
 215 220 225
 Tyr Ile Phe Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr
 230 235 240
 Lys Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu
 245 250 255
 Ser Leu Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile
 260 265 270
 His Gln Trp Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser
 275 280 285
 Ala Val Val Arg Ile Phe Asn Leu Ile Gly Met Met Leu Leu Leu
 290 295 300
 Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val Pro Leu Leu Gln
 305 310 315
 Asp Phe Pro Pro Asp Cys Trp Val Ser Leu Asn Glu Met Val Asn
 320 325 330

Asp	Ser	Trp	Gly	Lys	Gln	Tyr	Ser	Tyr	Ala	Leu	Phe	Lys	Ala	Met
				335					340					345
Ser	His	Met	Leu	Cys	Ile	Gly	Tyr	Gly	Ala	Gln	Ala	Pro	Val	Ser
				350					355					360
Met	Ser	Asp	Leu	Trp	Ile	Thr	Met	Leu	Ser	Met	Ile	Val	Gly	Ala
				365					370					375
Thr	Cys	Tyr	Ala	Met	Phe	Val	Gly	His	Ala	Thr	Ala	Leu	Ile	Gln
				380					385					390
Ser	Leu	Asp	Ser	Ser	Arg	Arg	Gln	Tyr	Gln	Glu	Lys	Tyr	Lys	Gln
				395					400					405
Val	Glu	Gln	Tyr	Met	Ser	Phe	His	Lys	Leu	Pro	Ala	Asp	Met	Arg
				410					415					420
Gln	Lys	Ile	His	Asp	Tyr	Tyr	Glu	His	Arg	Tyr	Gln	Gly	Lys	Ile
				425					430					435
Phe	Asp	Glu	Glu	Asn	Ile	Leu	Asn	Glu	Leu	Asn	Asp	Pro	Leu	Arg
				440					445					450
Glu	Glu	Ile	Val	Asn	Phe	Asn	Cys	Arg	Lys	Leu	Val	Ala	Thr	Met
				455					460					465
Pro	Leu	Phe	Ala	Asn	Ala	Asp	Pro	Asn	Phe	Val	Thr	Ala	Met	Leu
				470					475					480
Ser	Lys	Leu	Arg	Phe	Glu	Val	Phe	Gln	Pro	Gly	Asp	Tyr	Ile	Ile
				485					490					495
Arg	Glu	Gly	Ala	Val	Gly	Lys	Lys	Met	Tyr	Phe	Ile	Gln	His	Gly
				500					505					510
Val	Ala	Gly	Val	Ile	Thr	Lys	Ser	Ser	Lys	Glu	Met	Lys	Leu	Thr
				515					520					525
Asp	Gly	Ser	Tyr	Phe	Gly	Glu	Ile	Cys	Leu	Leu	Thr	Lys	Gly	Arg
				530					535					540
Arg	Thr	Ala	Ser	Val	Arg	Ala	Asp	Thr	Tyr	Cys	Arg	Leu	Tyr	Ser
				545					550					555
Leu	Ser	Val	Asp	Asn	Phe	Asn	Glu	Val	Leu	Glu	Glu	Tyr	Pro	Met
				560					565					570
Met	Arg	Arg	Ala	Phe	Glu	Thr	Val	Ala	Ile	Asp	Arg	Leu	Asp	Arg
				575					580					585
Ile	Gly	Lys	Lys	Asn	Ser	Ile	Leu	Leu	Gln	Lys	Phe	Gln	Lys	Asp
				590					595					600
Leu	Asn	Thr	Gly	Val	Phe	Asn	Asn	Gln	Glu	Asn	Glu	Ile	Leu	Lys
				605					610					615
Gln	Ile	Val	Lys	His	Asp	Arg	Glu	Met	Val	Gln	Ala	Ile	Ala	Pro
				620					625					630
Ile	Asn	Tyr	Pro	Gln	Met	Thr	Thr	Leu	Asn	Ser	Thr	Ser	Ser	Thr
				635					640					645
Thr	Thr	Pro	Thr	Ser	Arg	Met	Arg	Thr	Gln	Ser	Pro	Pro	Val	Tyr
				650					655					660
Thr	Ala	Thr	Ser	Leu	Ser	His	Ser	Asn	Leu	His	Ser	Pro	Ser	Pro
				665					670					675
Ser	Thr	Gln	Thr	Pro	Gln	Pro	Ser	Ala	Ile	Leu	Ser	Pro	Cys	Ser
				680					685					690
Tyr	Thr	Thr	Ala	Val	Cys	Ser	Pro	Pro	Val	Gln	Ser	Pro	Leu	Ala
				695					700					705
Ala	Arg	Thr	Phe	His	Tyr	Ala	Ser	Pro	Thr	Ala	Ser	Gln	Leu	Ser
				710					715					720
Leu	Met	Gln	Gln	Gln	Pro	Gln	Gln	Gln	Val	Gln	Gln	Ser	Gln	Pro
				725					730					735
Pro	Gln	Thr	Gln	Pro	Gln	Gln	Pro	Ser	Pro	Gln	Pro	Gln	Thr	Pro
				740					745					750
Gly	Ser	Ser	Thr	Pro	Lys	Asn	Glu	Val	His	Lys	Ser	Thr	Gln	Ala
				755					760					765
Leu	His	Asn	Thr	Asn	Leu	Thr	Arg	Glu	Val	Arg	Pro	Leu	Ser	Ala
				770					775					780
Ser	Gln	Pro	Ser	Leu	Pro	His	Glu	Val	Ser	Thr	Leu	Ile	Ser	Arg
				785					790					795
Pro	His	Pro	Thr	Val	Gly	Glu	Ser	Leu	Ala	Ser	Ile	Pro	Gln	Pro

	800		805		810
Val Thr Ala Val	Pro Gly Thr Gly Leu	Gln Ala Gly Gly Arg Ser			
	815		820		825
Thr Val Pro Gln	Arg Val Thr Leu Phe	Arg Gln Met Ser Ser Gly			
	830		835		840
Ala Ile Pro Pro	Asn Arg Gly Val Pro	Pro Ala Pro Pro Pro Pro			
	845		850		855
Ala Ala Ala Leu	Pro Arg Glu Ser Ser	Ser Val Leu Asn Thr Asp			
	860		865		870
Pro Asp Ala Glu	Lys Pro Arg Phe Ala	Ser Asn Leu			
	875		880		

<210> 12

<211> 1547

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7480632CD1

<400> 12

Met Val Lys Lys Glu Ile Ser Val Arg Gln Gln Ile Gln Ala Leu		
1	5	10
Leu Tyr Lys Asn Phe Leu Lys Lys Trp Arg Ile Lys Arg Glu Phe		
	20	25
Leu Glu Glu Trp Thr Ile Thr Leu Phe Leu Gly Leu Tyr Leu Cys		
	35	40
Ile Phe Ser Glu His Phe Arg Ala Thr Arg Phe Pro Glu Gln Pro		
	50	55
Pro Lys Val Leu Gly Ser Val Asp Gln Phe Asn Asp Ser Gly Leu		
	65	70
Val Val Ala Tyr Thr Pro Val Ser Asn Ile Thr Gln Arg Ile Met		
	80	85
Asn Lys Met Ala Leu Ala Ser Phe Met Lys Gly Arg Thr Val Ile		
	95	100
Gly Thr Pro Asp Glu Glu Thr Met Asp Ile Glu Leu Pro Lys Lys		
	110	115
Tyr His Glu Met Val Gly Val Ile Phe Ser Asp Thr Phe Ser Tyr		
	125	130
Arg Leu Lys Phe Asn Trp Gly Tyr Arg Ile Pro Val Ile Lys Glu		
	140	145
His Ser Glu Tyr Thr Gly His Cys Trp Ala Met His Gly Glu Ile		
	155	160
Phe Cys Tyr Leu Ala Lys Tyr Trp Leu Lys Gly Phe Val Ala Phe		
	170	175
Gln Ala Ala Ile Asn Ala Ala Ile Ile Glu Val Thr Thr Asn His		
	185	190
Ser Val Met Glu Glu Leu Thr Ser Val Ile Gly Ile Asn Met Lys		
	200	205
Ile Pro Pro Phe Ile Ser Lys Gly Glu Ile Met Asn Glu Trp Phe		
	215	220
His Phe Thr Cys Leu Val Ser Phe Ser Ser Phe Ile Tyr Phe Ala		
	230	235
Ser Leu Asn Val Ala Arg Glu Arg Gly Lys Phe Lys Lys Leu Met		
	245	250
Thr Val Met Gly Leu Arg Glu Ser Ala Phe Trp Leu Ser Trp Gly		
	260	265
Leu Thr Tyr Ile Cys Phe Ile Phe Ile Met Ser Ile Phe Met Ala		
	275	280
Leu Val Ile Thr Ser Ile Pro Ile Val Phe His Thr Gly Phe Met		
	290	295
Val Ile Phe Thr Leu Tyr Ser Leu Tyr Gly Leu Ser Leu Val Ala		

	305	310	315
Leu Ala Phe Leu	Met Ser Val Leu Ile	Arg Lys Pro Met Leu	Ala
	320	325	330
Gly Leu Ala Gly	Phe Leu Phe Thr Val	Phe Trp Gly Cys Leu	Gly
	335	340	345
Phe Thr Val Leu	Tyr Arg Gln Leu Pro	Leu Ser Leu Gly Trp	Val
	350	355	360
Leu Ser Leu Leu	Ser Pro Phe Ala Phe	Thr Ala Gly Met Ala	Gln
	365	370	375
Ile Thr His Leu	Asp Asn Tyr Leu Ser	Gly Val Ile Phe Pro	Asp
	380	385	390
Pro Ser Gly Asp	Ser Tyr Lys Met Ile	Ala Thr Phe Phe Ile	Leu
	395	400	405
Ala Phe Asp Thr	Leu Phe Tyr Leu Ile	Phe Thr Leu Tyr Phe	Glu
	410	415	420
Arg Val Leu Pro	Gly Lys Asp Gly His	Gly Asp Ser Pro Leu	Phe
	425	430	435
Phe Leu Lys Ser	Ser Phe Trp Ser Lys	His Gln Asn Thr His	His
	440	445	450
Glu Ile Phe Glu	Asn Glu Ile Asn Pro	Glu His Ser Ser Asp	Asp
	455	460	465
Ser Phe Glu Pro	Val Ser Pro Glu Phe	His Gly Lys Glu Ala	Ile
	470	475	480
Arg Ile Arg Asn	Val Ile Lys Glu Tyr	Asn Gly Lys Thr Gly	Lys
	485	490	495
Val Glu Ala Leu	Gln Gly Ile Phe Phe	Asp Ile Tyr Glu Gly	Gln
	500	505	510
Ile Thr Ala Ile	Leu Gly His Asn Gly	Ala Gly Lys Ser Thr	Leu
	515	520	525
Leu Asn Ile Leu	Ser Gly Leu Ser Val	Ser Thr Glu Gly Ser	Ala
	530	535	540
Thr Ile Tyr Asn	Thr Gln Leu Ser Glu	Ile Thr Asp Met Glu	Glu
	545	550	555
Ile Arg Lys Asn	Ile Gly Phe Cys Pro	Gln Phe Asn Phe Gln	Phe
	560	565	570
Asp Phe Leu Thr	Val Arg Glu Asn Leu	Arg Val Phe Ala Lys	Ile
	575	580	585
Lys Gly Ile Gln	Pro Lys Glu Val Glu	Gln Glu Val Leu Leu	Leu
	590	595	600
Asp Glu Pro Thr	Ala Gly Leu Asp Pro	Phe Ser Arg His Arg	Val
	605	610	615
Trp Ser Leu Leu	Lys Glu His Lys Val	Asp Arg Leu Ile Leu	Phe
	620	625	630
Ser Thr Gln Phe	Met Asp Glu Ala Asp	Ile Leu Ala Asp Arg	Lys
	635	640	645
Val Phe Leu Ser	Asn Gly Lys Leu Lys	Cys Ala Gly Ser Ser	Leu
	650	655	660
Phe Leu Lys Arg	Lys Trp Gly Ile Gly	Tyr His Leu Ser Leu	His
	665	670	675
Arg Asn Glu Met	Cys Asp Thr Glu Lys	Ile Thr Ser Leu Ile	Lys
	680	685	690
Gln His Ile Pro	Asp Ala Lys Leu Thr	Thr Glu Ser Glu Glu	Lys
	695	700	705
Leu Val Tyr Ser	Leu Pro Leu Glu Lys	Thr Asn Lys Phe Pro	Asp
	710	715	720
Leu Tyr Ser Asp	Leu Asp Lys Cys Ser	Asp Gln Gly Ile Arg	Asn
	725	730	735
Tyr Ala Val Ser	Val Thr Ser Leu Asn	Glu Val Phe Leu Asn	Leu
	740	745	750
Glu Gly Lys Ser	Ala Ile Asp Glu Pro	Asp Phe Asp Ile Gly	Lys
	755	760	765
Gln Glu Lys Ile	His Val Thr Arg Asn	Thr Gly Asp Glu Ser	Glu
	770	775	780

Met Glu Gln Val	Leu Cys Ser Leu Pro	Glu Thr Arg Lys Ala Val	785	790	795
Ser Ser Ala Ala	Leu Trp Arg Arg Gln	Ile Tyr Ala Val Ala Thr	800	805	810
Leu Arg Phe Leu	Lys Leu Arg Arg Glu	Arg Arg Ala Leu Leu Cys	815	820	825
Leu Leu Leu Val	Leu Gly Ile Ala Phe	Ile Pro Ile Ile Leu Glu	830	835	840
Lys Ile Met Tyr	Lys Val Thr Arg Glu	Thr His Cys Trp Glu Phe	845	850	855
Ser Pro Ser Met	Tyr Phe Leu Ser Leu	Glu Gln Ile Pro Lys Thr	860	865	870
Pro Leu Thr Ser	Leu Leu Ile Val Asn	Asn Thr Gly Ser Asn Ile	875	880	885
Glu Asp Leu Val	His Ser Leu Lys Cys	Gln Asp Ile Val Leu Glu	890	895	900
Ile Asp Asp Phe	Arg Asn Arg Asn Gly	Ser Asp Asp Pro Ser Tyr	905	910	915
Asn Gly Ala Ile	Ile Val Ser Gly Asp	Gln Lys Asp Tyr Arg Phe	920	925	930
Ser Val Ala Cys	Asn Thr Lys Lys Leu	Asn Cys Phe Pro Val Leu	935	940	945
Met Gly Ile Val	Ser Asn Ala Leu Met	Gly Ile Phe Asn Phe Thr	950	955	960
Glu Leu Ile Gln	Met Glu Ser Thr Ser	Phe Phe Phe Tyr Ile Thr	965	970	975
Thr Lys Ser Phe	Gln Thr Lys Ile Pro	Ser Ser Ile Pro Ser Ile	980	985	990
Leu Cys Gln Lys	Asn Val Gln Ser Gln	Leu Trp Ile Ser Gly Leu	995	1000	1005
Trp Pro Ser Ala	Tyr Trp Cys Gly Gln	Ala Leu Val Asp Ile Pro	1010	1015	1020
Leu Tyr Phe Leu	Ile Leu Phe Ser Ile	His Leu Ile Tyr Tyr Phe	1025	1030	1035
Ile Phe Leu Gly	Phe Gln Leu Ser Trp	Glu Leu Met Phe Val Leu	1040	1045	1050
Val Val Cys Ile	Ile Gly Cys Ala Val	Ser Leu Ile Phe Leu Thr	1055	1060	1065
Tyr Val Leu Ser	Phe Ile Phe Arg Lys	Trp Arg Lys Asn Asn Gly	1070	1075	1080
Phe Trp Ser Phe	Gly Phe Phe Ile Val	Ser Ile Tyr Thr Asp Phe	1085	1090	1095
Ser Phe His Tyr	Asn Val Ser Arg Cys	Asp Phe Leu Phe Ile Phe	1100	1105	1110
Ile Phe Val Cys	Leu Phe Ile Ala His	His Phe Ser Phe Cys Ser	1115	1120	1125
Pro Tyr Leu Gln	Ser Val Ile Phe Leu	Phe Val Ile Arg Cys Leu	1130	1135	1140
Glu Met Lys Tyr	Gly Asn Glu Ile Met	Asn Lys Asp Pro Val Phe	1145	1150	1155
Arg Ile Ser Pro	Arg Ser Arg Glu Thr	His Pro Asn Pro Glu Glu	1160	1165	1170
Pro Glu Glu Glu	Asp Glu Asp Val Gln	Ala Glu Arg Val Gln Ala	1175	1180	1185
Ala Asn Ala Leu	Thr Ala Pro Asn Leu	Glu Glu Glu Pro Val Ile	1190	1195	1200
Thr Ala Ser Cys	Leu His Lys Glu Tyr	Tyr Glu Thr Lys Lys Ser	1205	1210	1215
Cys Phe Ser Thr	Arg Lys Lys Lys Ile	Ala Ile Arg Asn Val Ser	1220	1225	1230
Phe Cys Val Lys	Lys Gly Glu Val Leu	Gly Leu Leu Gly His Asn	1235	1240	1245
Gly Ala Gly Lys	Ser Thr Ser Ile Lys	Met Ile Thr Gly Cys Thr			

1250	1255	1260
Lys Pro Thr Ala Gly Val Val Val Leu Gln Gly Ser Arg Ala Ser		
1265	1270	1275
Val Arg Gln Gln His Asp Asn Ser Leu Lys Phe Leu Gly Tyr Cys		
1280	1285	1290
Pro Gln Glu Asn Ser Leu Trp Pro Lys Leu Thr Met Lys Glu His		
1295	1300	1305
Leu Glu Leu Tyr Ala Ala Val Lys Gly Leu Gly Lys Glu Asp Ala		
1310	1315	1320
Ala Leu Ser Ile Ser Arg Leu Val Glu Ala Leu Lys Leu Gln Glu		
1325	1330	1335
Gln Leu Lys Ala Pro Val Lys Thr Leu Ser Glu Gly Ile Lys Arg		
1340	1345	1350
Lys Leu Cys Phe Val Leu Ser Ile Leu Gly Asn Pro Ser Val Val		
1355	1360	1365
Leu Leu Asp Glu Pro Phe Thr Gly Met Asp Pro Glu Gly Gln Gln		
1370	1375	1380
Gln Met Trp Gln Ile Leu Gln Ala Thr Val Lys Asn Lys Glu Arg		
1385	1390	1395
Gly Thr Leu Leu Thr Thr His Tyr Met Ser Glu Ala Glu Ala Val		
1400	1405	1410
Cys Asp Arg Met Ala Met Met Val Ser Gly Thr Leu Arg Cys Ile		
1415	1420	1425
Gly Ser Ile Gln His Leu Lys Asn Lys Phe Gly Arg Asp Tyr Leu		
1430	1435	1440
Leu Glu Ile Lys Met Lys Glu Pro Thr Gln Val Glu Ala Leu His		
1445	1450	1455
Thr Glu Ile Leu Lys Leu Phe Pro Gln Ala Ala Trp Gln Glu Arg		
1460	1465	1470
Tyr Ser Ser Leu Met Ala Tyr Lys Leu Pro Val Glu Asp Val His		
1475	1480	1485
Pro Leu Ser Arg Ala Phe Phe Lys Leu Glu Ala Met Lys Gln Thr		
1490	1495	1500
Phe Asn Leu Glu Glu Tyr Ser Leu Ser Gln Ala Thr Leu Glu Gln		
1505	1510	1515
Val Phe Leu Glu Leu Cys Lys Glu Gln Glu Leu Gly Asn Val Asp		
1520	1525	1530
Asp Lys Ile Asp Thr Thr Val Glu Trp Lys Leu Leu Pro Gln Glu		
1535	1540	1545
Asp Pro		

<210> 13
 <211> 698
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 6952742CD1

<400> 13
 Met Asp Glu Ser Pro Glu Pro Leu Gln Gln Gly Arg Gly Pro Val
 1 5 10 15
 Pro Val Arg Arg Gln Arg Pro Ala Pro Arg Gly Leu Arg Glu Met
 20 25 30
 Leu Lys Ala Arg Leu Trp Cys Ser Cys Ser Cys Ser Val Leu Cys
 35 40 45
 Val Arg Ala Leu Val Gln Asp Leu Leu Pro Ala Thr Arg Trp Leu
 50 55 60
 Arg Gln Tyr Arg Pro Arg Glu Tyr Leu Ala Gly Asp Val Met Ser
 65 70 75
 Gly Leu Val Ile Gly Ile Ile Leu Ala Ile Ala Tyr Ser Leu Leu

	80		85		90
Ala Gly Leu Gln Pro Ile Tyr Ser Leu Tyr Thr Ser Phe Phe Ala					
	95		100		105
Asn Leu Ile Tyr Phe Leu Met Gly Thr Ser Arg His Val Ser Val					
	110		115		120
Gly Ile Phe Ser Leu Leu Cys Leu Met Val Gly Gln Val Val Asp					
	125		130		135
Arg Glu Leu Gln Leu Ala Gly Phe Asp Pro Ser Gln Asp Gly Leu					
	140		145		150
Gln Pro Gly Ala Asn Ser Ser Thr Leu Asn Gly Ser Ala Ala Met					
	155		160		165
Leu Asp Cys Gly Arg Asp Cys Tyr Ala Ile Arg Val Ala Thr Ala					
	170		175		180
Leu Thr Leu Met Thr Gly Leu Tyr Gln Val Leu Met Gly Val Leu					
	185		190		195
Arg Leu Gly Phe Val Ser Ala Tyr Leu Ser Gln Pro Leu Leu Asp					
	200		205		210
Gly Phe Ala Met Gly Ala Ser Val Thr Ile Leu Thr Ser Gln Leu					
	215		220		225
Lys His Leu Leu Gly Val Arg Ile Pro Arg His Gln Gly Pro Gly					
	230		235		240
Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg Gly Ala Gly Gln					
	245		250		255
Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys Leu Ala Val					
	260		265		270
Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His Arg Leu					
	275		280		285
Arg Val Pro Leu Pro Thr Glu Leu Leu Val Ile Val Val Ala Thr					
	290		295		300
Leu Val Ser His Phe Gly Gln Leu His Lys Arg Phe Gly Ser Ser					
	305		310		315
Val Ala Gly Asp Ile Pro Thr Gly Phe Met Pro Pro Gln Val Pro					
	320		325		330
Glu Pro Arg Leu Met Gln Arg Val Ala Leu Asp Ala Val Ala Leu					
	335		340		345
Ala Leu Val Ala Ala Ala Phe Ser Ile Ser Leu Ala Glu Met Phe					
	350		355		360
Ala Arg Ser His Gly Tyr Ser Val Arg Ala Asn Gln Glu Leu Leu					
	365		370		375
Ala Val Gly Cys Cys Asn Val Leu Pro Ala Phe Leu His Cys Phe					
	380		385		390
Ala Thr Ser Ala Ala Leu Ala Lys Ser Leu Val Lys Thr Ala Thr					
	395		400		405
Gly Cys Arg Thr Gln Leu Ser Ser Val Val Ser Ala Thr Val Val					
	410		415		420
Leu Leu Val Leu Leu Ala Leu Ala Pro Leu Phe His Asp Leu Gln					
	425		430		435
Arg Ser Val Leu Ala Cys Val Ile Val Val Ser Leu Arg Gly Ala					
	440		445		450
Leu Arg Lys Val Trp Asp Leu Pro Arg Leu Trp Arg Met Ser Pro					
	455		460		465
Ala Asp Ala Leu Val Trp Ala Gly Thr Val Ala Thr Cys Met Leu					
	470		475		480
Val Ser Thr Glu Ala Gly Leu Leu Ala Gly Val Ile Leu Ser Leu					
	485		490		495
Leu Ser Leu Ala Gly Arg Thr Gln Ser His Gly Thr Ala Leu Leu					
	500		505		510
Ala Arg Ile Gly Asp Thr Ala Phe Tyr Glu Asp Ala Thr Glu Phe					
	515		520		525
Glu Gly Leu Val Pro Glu Pro Gly Val Arg Val Phe Arg Phe Gly					
	530		535		540
Gly Pro Leu Tyr Tyr Ala Asn Lys Asp Phe Phe Leu Gln Ser Leu					
	545		550		555

Tyr	Ser	Leu	Thr	Gly	Leu	Asp	Ala	Gly	Cys	Met	Ala	Ala	Arg	Arg	
				560					565					570	
Lys	Glu	Gly	Gly	Ser	Glu	Thr	Gly	Val	Gly	Glu	Gly	Gly	Pro	Ala	
				575					580					585	
Gln	Gly	Glu	Asp	Leu	Gly	Pro	Val	Ser	Thr	Arg	Ala	Ala	Leu	Val	
				590					595					600	
Pro	Ala	Ala	Ala	Gly	Phe	His	Thr	Val	Val	Ile	Asp	Cys	Ala	Pro	
				605					610					615	
Leu	Leu	Phe	Leu	Asp	Ala	Ala	Gly	Val	Ser	Thr	Leu	Gln	Asp	Leu	
				620					625					630	
Arg	Arg	Asp	Tyr	Gly	Ala	Leu	Gly	Ile	Ser	Leu	Leu	Leu	Ala	Cys	
				635					640					645	
Cys	Ser	Pro	Pro	Val	Arg	Asp	Ile	Leu	Ser	Arg	Gly	Gly	Phe	Leu	
				650					655					660	
Gly	Glu	Gly	Pro	Gly	Asp	Thr	Ala	Glu	Glu	Glu	Gln	Leu	Phe	Leu	
				665					670					675	
Ser	Val	His	Asp	Ala	Val	Gln	Thr	Ala	Arg	Ala	Arg	His	Arg	Glu	
				680					685					690	
Leu	Glu	Ala	Thr	Asp	Ala	His	Leu								
				695											

<210> 14

<211> 766

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7478795CD1

<400> 14

Met	Arg	Leu	Trp	Lys	Ala	Val	Val	Val	Thr	Leu	Ala	Phe	Met	Ser	
1				5					10					15	
Val	Asp	Ile	Cys	Val	Thr	Thr	Ala	Ile	Tyr	Val	Phe	Ser	His	Leu	
				20					25					30	
Asp	Arg	Ser	Leu	Leu	Glu	Asp	Ile	Arg	His	Phe	Asn	Ile	Phe	Asp	
				35					40					45	
Ser	Val	Leu	Asp	Leu	Trp	Ala	Ala	Cys	Leu	Tyr	Arg	Ser	Cys	Leu	
				50					55					60	
Leu	Leu	Gly	Ala	Thr	Ile	Gly	Val	Ala	Lys	Asn	Ser	Ala	Leu	Gly	
				65					70					75	
Pro	Arg	Arg	Leu	Arg	Ala	Ser	Trp	Leu	Val	Ile	Thr	Leu	Val	Cys	
				80					85					90	
Leu	Phe	Val	Gly	Ile	Tyr	Ala	Met	Val	Lys	Leu	Leu	Leu	Phe	Ser	
				95					100					105	
Glu	Val	Arg	Arg	Pro	Ile	Arg	Asp	Pro	Trp	Phe	Trp	Ala	Leu	Phe	
				110					115					120	
Val	Trp	Thr	Tyr	Ile	Ser	Leu	Gly	Ala	Ser	Phe	Leu	Leu	Trp	Trp	
				125					130					135	
Leu	Leu	Ser	Thr	Val	Arg	Pro	Gly	Thr	Gln	Ala	Leu	Glu	Pro	Gly	
				140					145					150	
Ala	Ala	Thr	Glu	Ala	Glu	Gly	Phe	Pro	Gly	Ser	Gly	Arg	Pro	Pro	
				155					160					165	
Pro	Glu	Gln	Ala	Ser	Gly	Ala	Thr	Leu	Gln	Lys	Leu	Leu	Ser	Tyr	
				170					175					180	
Thr	Lys	Pro	Asp	Val	Ala	Phe	Leu	Val	Ala	Ala	Ser	Phe	Phe	Leu	
				185					190					195	
Ile	Val	Ala	Ala	Leu	Gly	Glu	Thr	Phe	Leu	Pro	Tyr	Tyr	Thr	Gly	
				200					205					210	
Arg	Ala	Ile	Asp	Gly	Ile	Val	Ile	Gln	Lys	Ser	Met	Asp	Gln	Phe	
				215					220					225	
Ser	Thr	Ala	Val	Val	Ile	Val	Cys	Leu	Leu	Ala	Ile	Gly	Ser	Ser	
				230					235					240	

Phe Ala Ala Gly	Ile Arg Gly Gly Ile	Phe Thr Leu Ile Phe Ala	245	250	255
Arg Leu Asn Ile	Arg Leu Arg Asn Cys	Leu Phe Arg Ser Leu Val	260	265	270
Ser Gln Glu Thr	Ser Phe Phe Asp Glu	Asn Arg Thr Gly Asp Leu	275	280	285
Ile Ser Arg Leu	Thr Ser Asp Thr Thr	Met Val Ser Asp Leu Val	290	295	300
Ser Gln Asn Ile	Asn Val Phe Leu Arg	Asn Thr Val Lys Val Thr	305	310	315
Gly Val Val Val	Phe Met Phe Ser Leu	Ser Trp Gln Leu Ser Leu	320	325	330
Val Thr Phe Met	Gly Phe Pro Ile Ile	Met Met Val Ser Asn Ile	335	340	345
Tyr Gly Lys Tyr	Tyr Lys Arg Leu Ser	Lys Glu Val Gln Asn Ala	350	355	360
Leu Ala Arg Ala	Ser Asn Thr Ala Glu	Glu Thr Ile Ser Ala Met	365	370	375
Lys Thr Val Arg	Ser Phe Ala Asn Glu	Glu Glu Glu Ala Glu Val	380	385	390
Tyr Leu Arg Lys	Leu Gln Gln Val Tyr	Lys Leu Asn Arg Lys Glu	395	400	405
Ala Ala Ala Tyr	Met Tyr Tyr Val Trp	Gly Ser Gly Leu Thr Leu	410	415	420
Leu Val Val Gln	Val Ser Ile Leu Tyr	Tyr Gly Gly His Leu Val	425	430	435
Ile Ser Gly Gln	Met Thr Ser Gly Asn	Leu Ile Ala Phe Ile Ile	440	445	450
Tyr Glu Phe Val	Leu Gly Asp Cys Met	Glu Ser Val Gly Ser Val	455	460	465
Tyr Ser Gly Leu	Met Gln Gly Val Gly	Ala Ala Glu Lys Val Phe	470	475	480
Glu Phe Ile Asp	Arg Gln Pro Thr Met	Val His Asp Gly Ser Leu	485	490	495
Ala Pro Asp His	Leu Glu Gly Arg Val	Asp Phe Glu Asn Val Thr	500	505	510
Phe Thr Tyr Arg	Thr Arg Pro His Thr	Gln Val Leu Gln Asn Val	515	520	525
Ser Phe Ser Leu	Ser Pro Gly Lys Val	Thr Ala Leu Val Gly Pro	530	535	540
Ser Gly Ser Gly	Lys Ser Ser Cys Val	Asn Ile Leu Glu Asn Phe	545	550	555
Tyr Pro Leu Glu	Gly Gly Arg Val Leu	Leu Asp Gly Lys Pro Ile	560	565	570
Ser Ala Tyr Asp	His Lys Tyr Leu His	Arg Val Ile Ser Leu Val	575	580	585
Ser Gln Glu Pro	Val Leu Phe Ala Arg	Ser Ile Thr Asp Asn Ile	590	595	600
Ser Tyr Gly Leu	Pro Thr Val Pro Phe	Glu Met Val Val Glu Ala	605	610	615
Ala Gln Lys Ala	Asn Ala His Gly Phe	Ile Met Glu Leu Gln Asp	620	625	630
Gly Tyr Ser Thr	Glu Thr Gly Glu Lys	Gly Ala Gln Leu Ser Gly	635	640	645
Gly Gln Lys Gln	Arg Val Ala Met Ala	Arg Ala Leu Val Arg Asn	650	655	660
Pro Pro Val Leu	Ile Leu Asp Glu Ala	Thr Ser Ala Leu Asp Ala	665	670	675
Glu Ser Glu Tyr	Leu Ile Gln Gln Ala	Ile His Gly Asn Leu Gln	680	685	690
Lys His Thr Val	Leu Ile Ile Ala His	Arg Leu Ser Thr Val Glu	695	700	705
His Ala His Leu	Ile Val Val Leu Asp	Lys Gly Arg Val Val Gln			

	710	715	720
Gln Gly Thr His	Gln Gln Leu Leu Ala	Gln Gly Gly Leu Tyr	Ala
	725	730	735
Lys Leu Val Gln	Arg Gln Met Leu Gly	Leu Gln Pro Ala Ala	Asp
	740	745	750
Phe Thr Ala Gly	His Asn Glu Pro Val	Ala Asn Gly Ser His	Lys
	755	760	765
Ala			

<210> 15

<211> 450

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 656293CD1

<400> 15

Met Gly Leu Arg Ser His His Leu Ser Leu Gly Leu Leu Leu Leu		
1	5	10
Phe Leu Leu Pro Ala Glu Cys Leu Gly Ala Glu Gly Arg Leu Ala		
	20	25
Leu Lys Leu Phe Arg Asp Leu Phe Ala Asn Tyr Thr Ser Ala Leu		
	35	40
Arg Pro Val Ala Asp Thr Asp Gln Thr Leu Asn Val Thr Leu Glu		
	50	55
Val Thr Leu Ser Gln Ile Ile Asp Met Asp Glu Arg Asn Gln Val		
	65	70
Leu Thr Leu Tyr Leu Trp Ile Arg Gln Glu Trp Thr Asp Ala Tyr		
	80	85
Leu Arg Trp Asp Pro Asn Ala Tyr Gly Gly Leu Asp Ala Ile Arg		
	95	100
Ile Pro Ser Ser Leu Val Trp Arg Pro Asp Ile Val Leu Tyr Asn		
	110	115
Lys Ala Asp Ala Gln Pro Pro Gly Ser Ala Ser Thr Asn Val Val		
	125	130
Leu Arg His Asp Gly Ala Val Arg Trp Asp Ala Pro Ala Ile Thr		
	140	145
Arg Ser Ser Cys Arg Val Asp Val Ala Ala Phe Pro Phe Asp Ala		
	155	160
Gln His Cys Gly Leu Thr Phe Gly Ser Trp Thr His Gly Gly His		
	170	175
Gln Leu Asp Val Arg Pro Arg Gly Ala Ala Ala Ser Leu Ala Asp		
	185	190
Phe Val Glu Asn Val Glu Trp Arg Val Leu Gly Met Pro Ala Arg		
	200	205
Arg Arg Val Leu Thr Tyr Gly Cys Cys Ser Glu Pro Tyr Pro Asp		
	215	220
Val Thr Phe Thr Leu Leu Leu Arg Arg Arg Ala Ala Ala Tyr Val		
	230	235
Cys Asn Leu Leu Leu Pro Cys Val Leu Ile Ser Leu Leu Ala Pro		
	245	250
Leu Ala Phe His Leu Pro Ala Asp Ser Gly Glu Lys Val Ser Leu		
	260	265
Gly Val Thr Val Leu Leu Ala Leu Thr Val Phe Gln Leu Leu Leu		
	275	280
Ala Glu Ser Met Pro Pro Ala Glu Ser Val Pro Leu Ile Gly Lys		
	290	295
Tyr Tyr Met Ala Thr Met Thr Met Val Thr Phe Ser Thr Ala Leu		
	305	310
Thr Ile Leu Ile Met Asn Leu His Tyr Cys Gly Pro Ser Val Arg		

	320		325		330
Pro Val Pro Ala	Trp Ala Arg Ala Leu	Leu Leu Gly His Leu	Ala		
	335		340		345
Arg Gly Leu Cys	Val Arg Glu Arg Gly	Glu Pro Cys Gly Gln	Ser		
	350		355		360
Arg Pro Pro Glu	Leu Ser Pro Ser Pro	Gln Ser Pro Glu Gly	Gly		
	365		370		375
Ala Gly Pro Pro	Ala Gly Pro Cys His	Glu Pro Arg Cys Leu	Cys		
	380		385		390
Arg Gln Glu Ala	Leu Leu His His Val	Ala Thr Ile Ala Asn	Thr		
	395		400		405
Phe Arg Ser His	Arg Ala Ala Gln Arg	Cys His Glu Asp Trp	Lys		
	410		415		420
Arg Leu Ala Arg	Val Met Asp Arg Phe	Phe Leu Ala Ile Phe	Phe		
	425		430		435
Ser Met Ala Leu	Val Met Ser Leu Leu	Val Leu Val Gln Ala	Leu		
	440		445		450

<210> 16

<211> 260

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7473957CD1

<400> 16

Met Pro Ile Leu Ala	Asn Leu Pro Gly Met	Ser Ser Pro Arg Ala	
1	5	10	15
Met Glu Phe Thr Ser	Ser Gly Ser Ala Asn	Thr Glu Thr Thr Lys	
	20	25	30
Val Thr Gly Ser Leu	Glu Thr Lys Tyr Arg	Trp Thr Glu Tyr Gly	
	35	40	45
Leu Thr Phe Thr Glu	Lys Trp Asn Thr Asp	Asn Thr Leu Gly Thr	
	50	55	60
Glu Ile Thr Val Glu	Asp Gln Leu Ala Arg	Gly Leu Lys Leu Thr	
	65	70	75
Phe Asp Ser Ser Phe	Ser Pro Asn Thr Gly	Lys Lys Asn Ala Lys	
	80	85	90
Ile Lys Thr Gly Tyr	Lys Arg Glu His Ile	Asn Leu Gly Cys Asp	
	95	100	105
Met Asp Phe Asp Ile	Ala Gly Pro Ser Ile	Arg Gly Ala Leu Val	
	110	115	120
Leu Gly Tyr Glu Gly	Trp Leu Ala Gly Tyr	Gln Met Asn Phe Glu	
	125	130	135
Thr Ala Lys Ser Arg	Val Thr Gln Ser Asn	Phe Ala Val Gly Tyr	
	140	145	150
Lys Thr Asp Glu Phe	Gln Leu His Thr Asn	Val Asn Asp Gly Thr	
	155	160	165
Glu Phe Gly Gly Ser	Ile Tyr Gln Lys Val	Asn Lys Lys Leu Glu	
	170	175	180
Thr Ala Val Asn Leu	Ala Trp Thr Ala Gly	Asn Ser Asn Thr Arg	
	185	190	195
Phe Gly Ile Ala Ala	Lys Tyr Gln Ile Asp	Pro Asp Ala Cys Phe	
	200	205	210
Ser Ala Lys Val Asn	Asn Ser Ser Leu Ile	Gly Leu Gly Tyr Thr	
	215	220	225
Gln Thr Leu Lys Pro	Gly Ile Lys Leu Thr	Leu Ser Ala Leu Leu	
	230	235	240
Asp Gly Lys Asn Val	Asn Ala Gly Gly His	Lys Leu Gly Leu Gly	
	245	250	255

Leu Glu Phe Gln Ala
260

<210> 17

<211> 506

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474111CD1

<400> 17

Met	Ser	Glu	Pro	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Leu	Glu	Lys	Ala	1	5	10	15
Leu	Gln	Thr	Pro	Ser	Val	Pro	Ala	Pro	Glu	Ser	Thr	Leu	Gly	Phe	20	25	30	35
Glu	Pro	Gly	Leu	Leu	Lys	Gly	Ala	Leu	Gly	Thr	Ala	Gln	Phe	Ile	40	45	50	55
Pro	Met	Ala	Gln	Gly	Arg	Thr	Arg	Glu	Gln	Ala	Ser	Arg	Arg	Trp	60	65	70	75
Ala	Pro	Arg	Ser	Pro	Ala	Leu	Arg	Thr	Pro	Pro	Arg	His	Tyr	Gly	80	85	90	95
Pro	Glu	Arg	Arg	Gly	Arg	Thr	Ala	Ser	Arg	Gly	Gly	Glu	Pro	Glu	100	105	110	115
Val	Gln	Gly	Gly	Ala	Pro	Gly	Asn	Pro	Ser	Pro	Ser	Lys	Pro	Gly	120	125	130	135
Ser	Pro	Gln	Gly	Val	Gly	Pro	Ala	Ala	Trp	Glu	Arg	Ala	Pro	Arg	140	145	150	155
Pro	Arg	Cys	Ala	Gln	Pro	Ser	Gly	Ala	Arg	Val	Gly	Glu	Arg	Thr	160	165	170	175
Gln	Pro	Arg	Ser	Gln	Pro	Val	Gly	Leu	Ser	Arg	Gly	Ala	Gly	Glu	180	185	190	195
Asp	Ser	Pro	Ala	Thr	Arg	Ser	Gly	Ala	Ala	Ser	Val	Val	Leu	Asn	200	205	210	215
Val	Gly	Gly	Ala	Arg	Tyr	Ser	Leu	Ser	Arg	Glu	Leu	Leu	Lys	Asp	220	225	230	235
Phe	Pro	Leu	Arg	Arg	Val	Ser	Arg	Leu	His	Gly	Cys	Arg	Ser	Glu	240	245	250	255
Arg	Asp	Val	Leu	Glu	Val	Cys	Asp	Asp	Tyr	Asp	Arg	Glu	Arg	Asn	260	265	270	275
Glu	Tyr	Phe	Phe	Asp	Arg	His	Ser	Glu	Ala	Phe	Gly	Phe	Ile	Leu	280	285	290	295
Leu	Tyr	Ala	Ala	Pro	Ser	Arg	Arg	Trp	Leu	Glu	Arg	Met	Arg	Arg	300	305	310	315
Thr	Phe	Glu	Glu	Pro	Thr	Ser	Ser	Leu	Ala	Ala	Gln	Ile	Leu	Ala	320	325	330	335
Ser	Val	Ser	Val	Val	Phe	Val	Ile	Val	Ser	Met	Val	Val	Leu	Cys	340	345	350	355
Ala	Ser	Thr	Leu	Pro	Asp	Trp	Arg	Asn	Ala	Ala	Ala	Asp	Asn	Arg	360	365	370	375
Ser	Leu	Asp	Asp	Arg	Ser	Arg	Ile	Ile	Glu	Ala	Ile	Cys	Ile	Gly				
Trp	Phe	Thr	Ala	Glu	Cys	Ile	Val	Arg	Phe	Ile	Val	Ser	Lys	Asn				
Lys	Cys	Glu	Phe	Val	Lys	Arg	Pro	Leu	Asn	Ile	Ile	Asp	Leu	Leu				
Ala	Ile	Thr	Pro	Tyr	Tyr	Ile	Ser	Val	Leu	Met	Thr	Val	Phe	Thr				
Gly	Glu	Asn	Ser	Gln	Leu	Gln	Arg	Ala	Gly	Val	Thr	Leu	Arg	Val				
Leu	Arg	Met	Met	Arg	Ile	Phe	Trp	Val	Ile	Lys	Leu	Ala	Arg	His				

Phe	Ile	Gly	Leu	Gln	Thr	Leu	Gly	Leu	Thr	Leu	Lys	Arg	Cys	Tyr	
				380					385					390	
Arg	Glu	Met	Val	Met	Leu	Leu	Val	Phe	Ile	Cys	Val	Ala	Met	Ala	
				395					400					405	
Ile	Phe	Ser	Ala	Leu	Ser	Gln	Leu	Leu	Glu	His	Gly	Leu	Asp	Leu	
				410					415					420	
Glu	Thr	Ser	Asn	Lys	Asp	Phe	Thr	Ser	Ile	Pro	Ala	Ala	Cys	Trp	
				425					430					435	
Trp	Val	Ile	Ile	Ser	Met	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Met	Tyr	
				440					445					450	
Pro	Ile	Thr	Val	Pro	Gly	Arg	Ile	Leu	Gly	Gly	Val	Cys	Val	Val	
				455					460					465	
Ser	Gly	Ile	Val	Leu	Leu	Ala	Leu	Pro	Ile	Thr	Phe	Ile	Tyr	His	
				470					475					480	
Ser	Phe	Val	Gln	Cys	Tyr	His	Glu	Leu	Lys	Phe	Arg	Ser	Ala	Arg	
				485					490					495	
Tyr	Ser	Arg	Ser	Leu	Ser	Thr	Glu	Phe	Leu	Asn					
				500					505						

<210> 18

<211> 506

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7480826CD1

<400> 18

Met	Lys	Lys	Ala	Glu	Met	Gly	Arg	Phe	Ser	Ile	Ser	Pro	Asp	Glu	
1				5					10					15	
Asp	Ser	Ser	Ser	Tyr	Ser	Ser	Asn	Ser	Asp	Phe	Asn	Tyr	Ser	Tyr	
				20					25					30	
Pro	Thr	Lys	Gln	Ala	Ala	Leu	Lys	Ser	His	Tyr	Ala	Asp	Val	Asp	
				35					40					45	
Pro	Glu	Asn	Gln	Asn	Phe	Leu	Leu	Glu	Ser	Asn	Leu	Gly	Lys	Lys	
				50					55					60	
Lys	Tyr	Glu	Thr	Glu	Phe	His	Pro	Gly	Thr	Thr	Ser	Phe	Gly	Met	
				65					70					75	
Ser	Val	Phe	Asn	Leu	Ser	Asn	Ala	Ile	Val	Gly	Ser	Gly	Ile	Leu	
				80					85					90	
Gly	Leu	Ser	Tyr	Ala	Met	Ala	Asn	Thr	Gly	Ile	Ala	Leu	Phe	Ile	
				95					100					105	
Ile	Leu	Leu	Thr	Phe	Val	Ser	Ile	Phe	Ser	Leu	Tyr	Ser	Val	His	
				110					115					120	
Leu	Leu	Leu	Lys	Thr	Ala	Asn	Glu	Gly	Gly	Ser	Leu	Leu	Tyr	Glu	
				125					130					135	
Gln	Leu	Gly	Tyr	Lys	Ala	Phe	Gly	Leu	Val	Gly	Lys	Leu	Ala	Ala	
				140					145					150	
Ser	Gly	Ser	Ile	Thr	Met	Gln	Asn	Ile	Gly	Ala	Met	Ser	Ser	Tyr	
				155					160					165	
Leu	Phe	Ile	Val	Lys	Tyr	Glu	Leu	Pro	Leu	Val	Ile	Gln	Ala	Leu	
				170					175					180	
Thr	Asn	Ile	Glu	Asp	Lys	Thr	Gly	Leu	Trp	Tyr	Leu	Asn	Gly	Asn	
				185					190					195	
Tyr	Leu	Val	Leu	Leu	Val	Ser	Leu	Val	Val	Ile	Leu	Pro	Leu	Ser	
				200					205					210	
Leu	Phe	Arg	Asn	Leu	Gly	Tyr	Leu	Gly	Tyr	Thr	Ser	Gly	Leu	Ser	
				215					220					225	
Leu	Leu	Cys	Met	Val	Phe	Phe	Leu	Ile	Val	Val	Ile	Cys	Lys	Lys	
				230					235					240	
Phe	Gln	Val	Pro	Cys	Pro	Val	Glu	Ala	Ala	Leu	Ile	Ile	Asn	Glu	
				245					250					255	

Thr	Ile	Asn	Thr	Thr	Leu	Thr	Gln	Pro	Thr	Ala	Leu	Val	Pro	Ala	
				260					265					270	
Leu	Ser	His	Asn	Val	Thr	Glu	Asn	Asp	Ser	Cys	Arg	Pro	His	Tyr	
				275					280					285	
Phe	Ile	Phe	Asn	Ser	Gln	Thr	Val	Tyr	Ala	Val	Pro	Ile	Leu	Ile	
				290					295					300	
Phe	Ser	Phe	Val	Cys	His	Pro	Ala	Val	Leu	Pro	Ile	Tyr	Glu	Glu	
				305					310					315	
Leu	Lys	Asp	Arg	Ser	Arg	Arg	Arg	Met	Met	Asn	Val	Ser	Lys	Ile	
				320					325					330	
Ser	Phe	Phe	Ala	Met	Phe	Leu	Met	Tyr	Leu	Leu	Ala	Ala	Leu	Phe	
				335					340					345	
Gly	Tyr	Leu	Thr	Phe	Tyr	Glu	His	Val	Glu	Ser	Glu	Leu	Leu	His	
				350					355					360	
Thr	Tyr	Ser	Ser	Ile	Leu	Gly	Thr	Asp	Ile	Leu	Leu	Leu	Ile	Val	
				365					370					375	
Arg	Leu	Ala	Val	Leu	Met	Ala	Val	Thr	Leu	Thr	Val	Pro	Val	Val	
				380					385					390	
Ile	Phe	Pro	Ile	Arg	Ser	Ser	Val	Thr	His	Leu	Leu	Cys	Ala	Ser	
				395					400					405	
Lys	Asp	Phe	Ser	Trp	Trp	Arg	His	Ser	Leu	Ile	Thr	Val	Ser	Ile	
				410					415					420	
Leu	Ala	Phe	Thr	Asn	Leu	Leu	Val	Ile	Phe	Val	Pro	Thr	Ile	Arg	
				425					430					435	
Asp	Ile	Phe	Gly	Phe	Ile	Gly	Ala	Ser	Ala	Ala	Ser	Met	Leu	Ile	
				440					445					450	
Phe	Ile	Leu	Pro	Ser	Ala	Phe	Tyr	Ile	Lys	Leu	Val	Lys	Lys	Glu	
				455					460					465	
Pro	Met	Lys	Ser	Val	Gln	Lys	Ile	Gly	Ala	Leu	Phe	Phe	Leu	Leu	
				470					475					480	
Ser	Gly	Val	Leu	Val	Met	Thr	Gly	Ser	Met	Ala	Leu	Ile	Val	Leu	
				485					490					495	
Asp	Trp	Val	His	Asn	Ala	Pro	Gly	Gly	Gly	His					
				500					505						

<210> 19

<211> 315

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 6025572CD1

<400> 19

Met	His	Arg	Glu	Pro	Ala	Lys	Lys	Lys	Ala	Glu	Lys	Arg	Leu	Phe	
1				5					10					15	
Asp	Ala	Ser	Ser	Phe	Gly	Lys	Asp	Leu	Leu	Ala	Gly	Gly	Val	Ala	
				20					25					30	
Ala	Ala	Val	Ser	Lys	Thr	Ala	Val	Ala	Pro	Ile	Glu	Arg	Val	Lys	
				35					40					45	
Leu	Leu	Leu	Gln	Val	Gln	Ala	Ser	Ser	Lys	Gln	Ile	Ser	Pro	Glu	
				50					55					60	
Ala	Arg	Tyr	Lys	Gly	Met	Val	Asp	Cys	Leu	Val	Arg	Ile	Pro	Arg	
				65					70					75	
Glu	Gln	Gly	Phe	Phe	Ser	Phe	Trp	Arg	Gly	Asn	Leu	Ala	Asn	Val	
				80					85					90	
Ile	Arg	Tyr	Phe	Pro	Thr	Gln	Ala	Leu	Asn	Phe	Ala	Phe	Lys	Asp	
				95					100					105	
Lys	Tyr	Lys	Gln	Leu	Phe	Met	Ser	Gly	Val	Asn	Lys	Glu	Lys	Gln	
				110					115					120	
Phe	Trp	Arg	Trp	Phe	Leu	Ala	Asn	Leu	Ala	Ser	Gly	Gly	Ala	Ala	
				125					130					135	

Gly	Ala	Thr	Ser	Leu	Cys	Val	Val	Tyr	Pro	Leu	Asp	Phe	Ala	Arg	
				140					145					150	
Thr	Arg	Leu	Gly	Val	Asp	Ile	Gly	Lys	Gly	Pro	Glu	Glu	Arg	Gln	
				155					160					165	
Phe	Lys	Gly	Leu	Gly	Asp	Cys	Ile	Met	Lys	Ile	Ala	Lys	Ser	Asp	
				170					175					180	
Gly	Ile	Ala	Gly	Leu	Tyr	Gln	Gly	Phe	Gly	Val	Ser	Val	Gln	Gly	
				185					190					195	
Ile	Ile	Val	Tyr	Arg	Ala	Ser	Tyr	Phe	Gly	Ala	Tyr	Asp	Thr	Val	
				200					205					210	
Lys	Gly	Leu	Leu	Pro	Lys	Pro	Lys	Lys	Thr	Pro	Phe	Leu	Val	Ser	
				215					220					225	
Phe	Phe	Ile	Ala	Gln	Val	Val	Thr	Thr	Cys	Ser	Gly	Ile	Leu	Ser	
				230					235					240	
Tyr	Pro	Phe	Asp	Thr	Val	Arg	Arg	Arg	Met	Met	Met	Gln	Ser	Gly	
				245					250					255	
Glu	Ala	Lys	Arg	Gln	Tyr	Lys	Gly	Thr	Leu	Asp	Cys	Phe	Val	Lys	
				260					265					270	
Ile	Tyr	Gln	His	Glu	Gly	Ile	Ser	Ser	Phe	Phe	Arg	Gly	Ala	Phe	
				275					280					285	
Ser	Asn	Val	Leu	Arg	Gly	Thr	Gly	Gly	Ala	Leu	Val	Leu	Val	Leu	
				290					295					300	
Tyr	Asp	Lys	Ile	Lys	Glu	Phe	Phe	His	Ile	Asp	Ile	Gly	Gly	Arg	
				305					310					315	

<210> 20

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5686561CD1

<400> 20

Met	Val	Pro	Ala	Gly	Trp	Val	Arg	Gly	Leu	Glu	Leu	Ser	Leu	Trp	
1				5					10					15	
Gly	Gly	Asp	Pro	Val	Val	Pro	Trp	Ser	Cys	Arg	Phe	Cys	Ser	Gln	
				20					25					30	
Gln	Asp	Asp	Gly	Gln	Asp	Arg	Glu	Arg	Leu	Thr	Tyr	Phe	Gln	Asn	
				35					40					45	
Leu	Pro	Glu	Ser	Leu	Thr	Ser	Leu	Leu	Val	Leu	Leu	Thr	Thr	Ala	
				50					55					60	
Asn	Asn	Pro	Asp	Val	Met	Ile	Pro	Ala	Tyr	Ser	Lys	Asn	Arg	Ala	
				65					70					75	
Tyr	Ala	Ile	Phe	Phe	Ile	Val	Phe	Thr	Val	Ile	Gly	Ser	Leu	Phe	
				80					85					90	
Leu	Met	Asn	Leu	Leu	Thr	Ala	Ile	Ile	Tyr	Ser	Gln	Phe	Arg	Gly	
				95					100					105	
Tyr	Leu	Met	Lys	Ser	Leu	Gln	Thr	Ser	Leu	Phe	Arg	Arg	Arg	Leu	
				110					115					120	
Gly	Thr	Arg	Ala	Ala	Phe	Glu	Val	Leu	Ser	Ser	Met	Val	Gly	Glu	
				125					130					135	
Gly	Gly	Ala	Phe	Pro	Gln	Ala	Val	Gly	Val	Lys	Pro	Gln	Asn	Leu	
				140					145					150	
Leu	Gln	Val	Leu	Gln	Lys	Val	Gln	Leu	Asp	Ser	Ser	His	Lys	Gln	
				155					160					165	
Ala	Met	Met	Glu	Lys	Val	Arg	Ser	Tyr	Asp	Ser	Val	Leu	Leu	Ser	
				170					175					180	
Ala	Glu	Glu	Phe	Gln	Lys	Leu	Phe	Asn	Glu	Leu	Asp	Arg	Ser	Val	
				185					190					195	
Val	Lys	Glu	His	Pro	Pro	Arg	Pro	Glu	Tyr	Gln	Ser	Pro	Phe	Leu	

	200		205		210
Gln Ser Ala Gln	Phe Leu Phe Gly His	Tyr Tyr Phe Asp Tyr	Leu		
	215	220			225
Gly Asn Leu Ile	Ala Leu Ala Asn Leu	Val Ser Ile Cys Val	Phe		
	230	235			240
Leu Val Leu Asp	Ala Asp Val Leu Pro	Ala Glu Arg Asp Asp	Phe		
	245	250			255
Ile Leu Gly Ile	Leu Asn Cys Val Phe	Ile Val Tyr Tyr Leu	Leu		
	260	265			270
Glu Met Leu Leu	Lys Val Phe Ala Leu	Gly Leu Arg Gly Tyr	Leu		
	275	280			285
Ser Tyr Pro Ser	Asn Val Phe Asp Gly	Leu Leu Thr Val Val	Leu		
	290	295			300
Leu Val Leu Glu	Ile Ser Thr Leu Ala	Val Tyr Arg Leu Pro	His		
	305	310			315
Pro Gly Trp Arg	Pro Glu Met Val Gly	Leu Leu Ser Leu Trp	Asp		
	320	325			330
Met Thr Arg Met	Leu Asn Met Leu Ile	Val Phe Arg Phe Leu	Arg		
	335	340			345
Ile Ile Pro Ser	Met Lys Pro Met Ala	Val Val Ala Ser Thr	Val		
	350	355			360
Leu Gly Leu Val	Gln Asn Met Arg Ala	Phe Gly Gly Ile Leu	Val		
	365	370			375
Val Val Tyr Tyr	Val Phe Ala Ile Ile	Gly Ile Asn Leu Phe	Arg		
	380	385			390
Gly Val Ile Val	Ala Leu Pro Gly Asn	Ser Ser Leu Ala Pro	Ala		
	395	400			405
Asn Gly Ser Ala	Pro Cys Gly Ser Phe	Glu Gln Leu Glu Tyr	Trp		
	410	415			420
Ala Asn Asn Phe	Asp Asp Phe Ala Ala	Ala Leu Val Thr Leu	Trp		
	425	430			435
Asn Leu Met Val	Val Asn Asn Trp Gln	Val Phe Leu Asp Ala	Tyr		
	440	445			450
Arg Arg Tyr Ser	Gly Pro Trp Ser Lys	Ile Tyr Phe Val Leu	Trp		
	455	460			465
Trp Leu Val Ser	Ser Val Ile Trp Val	Asn Leu Phe Leu Ala	Leu		
	470	475			480
Ile Leu Glu Asn	Phe Leu His Lys Trp	Asp Pro Arg Ser His	Leu		
	485	490			495
Gln Pro Leu Ala	Gly Thr Pro Glu Ala	Thr Tyr Gln Met Thr	Val		
	500	505			510
Glu Leu Leu Phe	Arg Asp Ile Leu Glu	Glu Pro Gly Glu Asp	Glu		
	515	520			525
Leu Thr Glu Arg	Leu Ser Gln His Pro	His Leu Trp Leu Cys	Arg		
	530	535			540

<210> 21

<211> 322

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1553725CD1

<400> 21

Met Glu Ala Asp	Leu Ser Gly Phe Asn	Ile Asp Ala Pro Arg	Trp
1	5	10	15
Asp Gln Arg Thr	Phe Leu Gly Arg Val	Lys His Phe Leu Asn	Ile
	20	25	30
Thr Asp Pro Arg	Thr Val Phe Val Ser	Glu Arg Glu Leu Asp	Trp
	35	40	45

Ala	Lys	Val	Met	Val	Glu	Lys	Ser	Arg	Met	Gly	Val	Val	Pro	Pro	
				50					55						60
Gly	Thr	Gln	Val	Glu	Gln	Leu	Leu	Tyr	Ala	Lys	Lys	Leu	Tyr	Asp	
				65					70						75
Ser	Ala	Phe	His	Pro	Asp	Thr	Gly	Glu	Lys	Met	Asn	Val	Ile	Gly	
				80					85						90
Arg	Met	Ser	Phe	Gln	Leu	Pro	Gly	Gly	Met	Ile	Ile	Thr	Gly	Phe	
				95					100						105
Met	Leu	Gln	Phe	Tyr	Arg	Thr	Met	Pro	Ala	Val	Ile	Phe	Trp	Gln	
				110					115						120
Trp	Val	Asn	Gln	Ser	Phe	Asn	Ala	Leu	Val	Asn	Tyr	Thr	Asn	Arg	
				125					130						135
Asn	Ala	Ala	Ser	Pro	Thr	Ser	Val	Arg	Gln	Met	Ala	Leu	Ser	Tyr	
				140					145						150
Phe	Thr	Ala	Thr	Thr	Thr	Ala	Val	Ala	Thr	Ala	Val	Gly	Met	Asn	
				155					160						165
Met	Leu	Thr	Lys	Lys	Ala	Pro	Pro	Leu	Val	Gly	Arg	Trp	Val	Pro	
				170					175						180
Phe	Ala	Ala	Val	Ala	Ala	Ala	Asn	Cys	Val	Asn	Ile	Pro	Met	Met	
				185					190						195
Arg	Gln	Gln	Glu	Leu	Ile	Lys	Gly	Ile	Cys	Val	Lys	Asp	Arg	Asn	
				200					205						210
Glu	Asn	Glu	Ile	Gly	His	Ser	Arg	Arg	Ala	Ala	Ala	Ile	Gly	Ile	
				215					220						225
Thr	Gln	Val	Val	Ile	Ser	Arg	Ile	Thr	Met	Ser	Ala	Pro	Gly	Met	
				230					235						240
Ile	Leu	Leu	Pro	Val	Ile	Met	Glu	Arg	Leu	Glu	Lys	Leu	His	Phe	
				245					250						255
Met	Gln	Lys	Val	Lys	Val	Leu	His	Ala	Pro	Leu	Gln	Val	Met	Leu	
				260					265						270
Ser	Gly	Cys	Phe	Leu	Ile	Phe	Met	Val	Pro	Val	Ala	Cys	Gly	Leu	
				275					280						285
Phe	Pro	Gln	Lys	Cys	Glu	Leu	Pro	Val	Ser	Tyr	Leu	Glu	Pro	Lys	
				290					295						300
Leu	Gln	Asp	Thr	Ile	Lys	Ala	Lys	Tyr	Gly	Glu	Leu	Glu	Pro	Tyr	
				305					310						315
Val	Tyr	Phe	Asn	Lys	Gly	Leu									
				320											

<210> 22

<211> 417

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1695770CD1

<400> 22

Met	Thr	Thr	Leu	Val	Pro	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Leu	Trp	
				5					10						15
Thr	Leu	Pro	Gly	Gln	Val	Leu	Leu	Arg	Val	Ala	Leu	Ala	Lys	Glu	
				20					25						30
Glu	Val	Lys	Ser	Gly	Thr	Lys	Gly	Ser	Gln	Pro	Met	Ser	Pro	Ser	
				35					40						45
Asp	Phe	Leu	Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	
				50					55						60
Arg	Ile	Arg	Pro	Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	
				65					70						75
Asn	Ile	Phe	Ile	Asn	Ser	Phe	Ser	Ser	Val	Thr	Lys	Thr	Thr	Met	
				80					85						90
Asp	Tyr	Arg	Val	Asn	Val	Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Pro	
				95					100						105

Arg	Leu	Ser	Tyr	Arg	Glu	Tyr	Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	
				110					115					120	
Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp	Lys	Pro	Asp	Leu	Phe	Phe	Ala	
				125					130					135	
Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Glu	Val	Thr	Thr	Asp	Asn	Lys	
				140					145					150	
Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val	Leu	Tyr	Ser	Ile	Arg	
				155					160					165	
Leu	Thr	Leu	Ile	Leu	Ser	Cys	Leu	Met	Asp	Leu	Lys	Asn	Phe	Pro	
				170					175					180	
Met	Asp	Ile	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser	Phe	Gly	Tyr	
				185					190					195	
Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu	Glu	Asp	Ala	Pro	Ala	
				200					205					210	
Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	Arg	
				215					220					225	
Asp	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	
				230					235					240	
Lys	Phe	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	
				245					250					255	
Gly	Tyr	Tyr	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	
				260					265					270	
Ile	Leu	Ser	Trp	Val	Ser	Phe	Trp	Ile	Asn	Met	Asp	Ala	Ala	Pro	
				275					280					285	
Ala	Arg	Val	Gly	Leu	Gly	Ile	Thr	Thr	Val	Leu	Thr	Met	Thr	Thr	
				290					295					300	
Gln	Ser	Ser	Gly	Ser	Arg	Ala	Ser	Leu	Pro	Lys	Val	Ser	Tyr	Val	
				305					310					315	
Lys	Ala	Ile	Asp	Ile	Trp	Met	Ala	Val	Cys	Leu	Leu	Phe	Val	Phe	
				320					325					330	
Ala	Ala	Leu	Leu	Glu	Tyr	Ala	Ala	Ile	Asn	Phe	Val	Ser	Arg	Gln	
				335					340					345	
His	Lys	Glu	Phe	Ile	Arg	Leu	Arg	Arg	Arg	Gln	Arg	Arg	Gln	Arg	
				350					355					360	
Leu	Glu	Glu	Asp	Ile	Ile	Gln	Glu	Ser	Arg	Phe	Tyr	Phe	Arg	Gly	
				365					370					375	
Tyr	Gly	Leu	Gly	His	Cys	Leu	Gln	Ala	Arg	Asp	Gly	Gly	Pro	Met	
				380					385					390	
Glu	Gly	Ser	Gly	Ile	Tyr	Ser	Pro	Gln	Pro	Pro	Ala	Pro	Leu	Leu	
				395					400					405	
Arg	Glu	Gly	Glu	Thr	Thr	Arg	Lys	Leu	Tyr	Val	Asp				
				410					415						

<210> 23

<211> 1864

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4672222CD1

<400> 23

Met	Ser	Gln	Lys	Ser	Trp	Ile	Glu	Ser	Thr	Leu	Thr	Lys	Arg	Glu	
1				5					10					15	
Cys	Val	Tyr	Ile	Ile	Pro	Ser	Ser	Lys	Asp	Pro	His	Arg	Cys	Leu	
				20					25					30	
Pro	Gly	Cys	Gln	Ile	Cys	Gln	Gln	Leu	Val	Arg	Cys	Phe	Cys	Gly	
				35					40					45	
Arg	Leu	Val	Lys	Gln	His	Ala	Cys	Phe	Thr	Ala	Ser	Leu	Ala	Met	
				50					55					60	
Lys	Tyr	Ser	Asp	Val	Lys	Leu	Gly	Asp	His	Phe	Asn	Gln	Ala	Ile	
				65					70					75	

Glu	Glu	Trp	Ser	Val	Glu	Lys	His	Thr	Glu	Gln	Ser	Pro	Thr	Asp	
				80					85						90
Ala	Tyr	Gly	Val	Ile	Asn	Phe	Gln	Gly	Gly	Ser	His	Ser	Tyr	Arg	
				95					100						105
Ala	Lys	Tyr	Val	Arg	Leu	Ser	Tyr	Asp	Thr	Lys	Pro	Glu	Val	Ile	
				110					115						120
Leu	Gln	Leu	Leu	Leu	Lys	Glu	Trp	Gln	Met	Glu	Leu	Pro	Lys	Leu	
				125					130						135
Val	Ile	Ser	Val	His	Gly	Gly	Met	Gln	Lys	Phe	Glu	Leu	His	Pro	
				140					145						150
Arg	Ile	Lys	Gln	Leu	Leu	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Val	
				155					160						165
Thr	Thr	Gly	Ala	Trp	Ile	Leu	Thr	Gly	Gly	Val	Asn	Thr	Gly	Val	
				170					175						180
Ala	Lys	His	Val	Gly	Asp	Ala	Leu	Lys	Glu	His	Ala	Ser	Arg	Ser	
				185					190						195
Ser	Arg	Lys	Ile	Cys	Thr	Ile	Gly	Ile	Ala	Pro	Trp	Gly	Val	Ile	
				200					205						210
Glu	Asn	Arg	Asn	Asp	Leu	Val	Gly	Arg	Asp	Val	Val	Ala	Pro	Tyr	
				215					220						225
Gln	Thr	Leu	Leu	Asn	Pro	Leu	Ser	Lys	Leu	Asn	Val	Leu	Asn	Asn	
				230					235						240
Leu	His	Ser	His	Phe	Ile	Leu	Val	Asp	Asp	Gly	Thr	Val	Gly	Lys	
				245					250						255
Tyr	Gly	Ala	Glu	Val	Arg	Leu	Arg	Arg	Glu	Leu	Glu	Lys	Thr	Ile	
				260					265						270
Asn	Gln	Gln	Arg	Ile	His	Ala	Arg	Ile	Gly	Gln	Gly	Val	Pro	Val	
				275					280						285
Val	Ala	Leu	Ile	Phe	Glu	Gly	Gly	Pro	Asn	Val	Ile	Leu	Thr	Val	
				290					295						300
Leu	Glu	Tyr	Leu	Gln	Glu	Ser	Pro	Pro	Val	Pro	Val	Val	Val	Cys	
				305					310						315
Glu	Gly	Thr	Gly	Arg	Ala	Ala	Asp	Leu	Leu	Ala	Tyr	Ile	His	Lys	
				320					325						330
Gln	Thr	Glu	Glu	Gly	Gly	Asn	Leu	Pro	Asp	Ala	Ala	Glu	Pro	Asp	
				335					340						345
Ile	Ile	Ser	Thr	Ile	Lys	Lys	Thr	Phe	Asn	Phe	Gly	Gln	Asn	Glu	
				350					355						360
Ala	Leu	His	Leu	Phe	Gln	Thr	Leu	Met	Glu	Cys	Met	Lys	Arg	Lys	
				365					370						375
Glu	Leu	Ile	Thr	Val	Phe	His	Ile	Gly	Ser	Asp	Glu	His	Gln	Asp	
				380					385						390
Ile	Asp	Val	Ala	Ile	Leu	Thr	Ala	Leu	Leu	Lys	Gly	Thr	Asn	Ala	
				395					400						405
Ser	Ala	Phe	Asp	Gln	Leu	Ile	Leu	Thr	Leu	Ala	Trp	Asp	Arg	Val	
				410					415						420
Asp	Ile	Ala	Lys	Asn	His	Val	Phe	Val	Tyr	Gly	Gln	Gln	Trp	Leu	
				425					430						435
Val	Gly	Ser	Leu	Glu	Gln	Ala	Met	Leu	Asp	Ala	Leu	Val	Met	Asp	
				440					445						450
Arg	Val	Ala	Phe	Val	Lys	Leu	Leu	Ile	Glu	Asn	Gly	Val	Ser	Met	
				455					460						465
His	Lys	Phe	Leu	Thr	Ile	Pro	Arg	Leu	Glu	Glu	Leu	Tyr	Asn	Thr	
				470					475						480
Lys	Gln	Gly	Pro	Thr	Asn	Pro	Met	Leu	Phe	His	Leu	Val	Arg	Asp	
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Val	Lys	Gln	Gly	Asn	Leu	Pro	Pro	Gly	Tyr	Lys	Ile	Thr	Leu	Ile	
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Asp	Ile	Gly	Leu	Val	Ile	Glu	Tyr	Leu	Met	Gly	Gly	Thr	Tyr	Arg	
				515					520						525
Cys	Thr	Tyr	Thr	Arg	Lys	Arg	Phe	Arg	Leu	Ile	Tyr	Asn	Ser	Leu	
				530					535						540
Gly	Gly	Asn	Asn	Arg	Arg	Ser	Gly	Arg	Asn	Thr	Ser	Ser	Ser	Thr	

Pro Gln Leu Arg	545	Lys Ser His Glu Ser	550	Phe Gly Asn Arg Ala	555
	560		565		570
Lys Lys Glu Lys	575	Met Arg His Asn His	580	Phe Ile Lys Thr Ala	Gln
	590		595		600
Pro Tyr Arg Pro	605	Lys Ile Asp Thr Val	610	Met Glu Glu Gly Lys	Lys
	620		625		630
Lys Arg Thr Lys	635	Asp Glu Ile Val Asp	640	Ile Asp Asp Pro Glu	Thr
	650		655		660
Lys Arg Phe Pro	665	Tyr Pro Leu Asn Glu	670	Leu Leu Ile Trp Ala	Cys
	680		685		690
Leu Met Lys Arg	695	Gln Val Met Ala Arg	700	Phe Leu Trp Gln His	Gly
	710		715		720
Glu Glu Ser Met	725	Ala Lys Ala Leu Val	730	Ala Cys Lys Ile Tyr	Arg
	740		745		750
Ser Met Ala Tyr	755	Glu Ala Lys Gln Ser	760	Asp Leu Val Asp Asp	Thr
	770		775		780
Ser Glu Glu Leu	785	Lys Gln Tyr Ser Asn	790	Asp Phe Gly Gln Leu	Ala
	800		805		810
Val Glu Leu Leu	815	Glu Gln Ser Phe Arg	820	Gln Asp Glu Thr Met	Ala
	830		835		840
Met Lys Leu Leu	845	Thr Tyr Glu Leu Lys	850	Asn Trp Ser Asn Ser	Thr
	860		865		870
Cys Leu Lys Leu	875	Ala Val Ser Ser Arg	880	Leu Arg Pro Phe Val	Ala
	890		895		900
His Thr Cys Thr	905	Gln Met Leu Leu Ser	910	Asp Met Trp Met Gly	Arg
	920		925		930
Leu Asn Met Arg	935	Lys Asn Ser Trp Tyr	940	Lys Val Ile Leu Ser	Ile
	950		955		960
Leu Val Pro Pro	965	Ala Ile Leu Leu Leu	970	Glu Tyr Lys Thr Lys	Ala
	980		985		990
Glu Met Ser His	995	Ile Pro Gln Ser Gln	1000	Asp Ala His Gln Met	Thr
	1010		1015		1020
Met Asp Asp Ser		Glu Asn Asn Phe Gln		Asn Ile Thr Glu Glu	Ile
Pro Met Glu Val		Phe Lys Glu Val Arg		Ile Leu Asp Ser Asn	Glu
Gly Lys Asn Glu		Met Glu Ile Gln Met		Lys Ser Lys Lys Leu	Pro
Ile Thr Arg Lys		Phe Tyr Ala Phe Tyr		His Ala Pro Ile Val	Lys
Phe Trp Phe Asn		Thr Leu Ala Tyr Leu		Gly Phe Leu Met Leu	Tyr
Thr Phe Val Val		Leu Val Gln Met Glu		Gln Leu Pro Ser Val	Gln
Glu Trp Ile Val		Ile Ala Tyr Ile Phe		Thr Tyr Ala Ile Glu	Lys
Val Arg Glu Ile		Phe Met Ser Glu Ala		Gly Lys Val Asn Gln	Lys
Ile Lys Val Trp		Phe Ser Asp Tyr Phe		Asn Ile Ser Asp Thr	Ile
Ala Ile Ile Ser		Phe Phe Ile Gly Phe		Gly Leu Arg Phe Gly	Ala
Lys Trp Asn Phe		Ala Asn Ala Tyr Asp		Asn His Val Phe Val	Ala
Gly Arg Leu Ile		Tyr Cys Leu Asn Ile		Ile Phe Trp Tyr Val	Arg
Leu Leu Asp Phe		Leu Ala Val Asn Gln		Gln Ala Gly Pro Tyr	Val
Met Met Ile Gly		Lys Met Val Ala Asn		Met Phe Tyr Ile Val	Val
Ile Met Ala Leu		Val Leu Leu Ser Phe		Gly Val Pro Arg Lys	Ala

Ile	Leu	Tyr	Pro	His	Glu	Ala	Pro	Ser	Trp	Thr	Leu	Ala	Lys	Asp
									1030					1035
Ile	Val	Phe	His	Pro	Tyr	Trp	Met	Ile	Phe	Gly	Glu	Val	Tyr	Ala
									1045					1050
Tyr	Glu	Ile	Asp	Val	Cys	Ala	Asn	Asp	Ser	Val	Ile	Pro	Gln	Ile
									1060					1065
Cys	Gly	Pro	Gly	Thr	Trp	Leu	Thr	Pro	Phe	Leu	Gln	Ala	Val	Tyr
									1075					1080
Leu	Phe	Val	Gln	Tyr	Ile	Ile	Met	Val	Asn	Leu	Leu	Ile	Ala	Phe
									1090					1095
Phe	Asn	Asn	Val	Tyr	Leu	Gln	Val	Lys	Ala	Ile	Ser	Asn	Ile	Val
									1105					1110
Trp	Lys	Tyr	Gln	Arg	Tyr	His	Phe	Ile	Met	Ala	Tyr	His	Glu	Lys
									1120					1125
Pro	Val	Leu	Pro	Pro	Pro	Leu	Ile	Ile	Leu	Ser	His	Ile	Val	Ser
									1135					1140
Leu	Phe	Cys	Cys	Ile	Cys	Lys	Arg	Arg	Lys	Lys	Asp	Lys	Thr	Ser
									1150					1155
Asp	Gly	Pro	Lys	Leu	Phe	Leu	Thr	Glu	Glu	Asp	Gln	Lys	Lys	Leu
									1165					1170
His	Asp	Phe	Glu	Glu	Gln	Cys	Val	Glu	Met	Tyr	Phe	Asn	Glu	Lys
									1180					1185
Asp	Asp	Lys	Phe	His	Ser	Gly	Ser	Glu	Glu	Arg	Ile	Arg	Val	Thr
									1195					1200
Phe	Glu	Arg	Val	Glu	Gln	Met	Cys	Ile	Gln	Ile	Lys	Glu	Val	Gly
									1210					1215
Asp	Arg	Val	Asn	Tyr	Ile	Lys	Arg	Ser	Leu	Gln	Ser	Leu	Asp	Ser
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Gln	Ile	Gly	His	Leu	Gln	Asp	Leu	Ser	Ala	Leu	Thr	Val	Asp	Thr
									1240					1245
Leu	Lys	Thr	Leu	Thr	Ala	Gln	Lys	Ala	Ser	Glu	Ala	Ser	Lys	Val
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His	Asn	Glu	Ile	Thr	Arg	Glu	Leu	Ser	Ile	Ser	Lys	His	Leu	Ala
									1270					1275
Gln	Asn	Leu	Ile	Asp	Asp	Gly	Pro	Val	Arg	Pro	Ser	Val	Trp	Lys
									1285					1290
Lys	His	Gly	Val	Val	Asn	Thr	Leu	Ser	Ser	Ser	Leu	Pro	Gln	Gly
									1300					1305
Asp	Leu	Glu	Ser	Asn	Asn	Pro	Phe	His	Cys	Asn	Ile	Leu	Met	Lys
									1315					1320
Asp	Asp	Lys	Asp	Pro	Gln	Cys	Asn	Ile	Phe	Gly	Gln	Asp	Leu	Pro
									1330					1335
Ala	Val	Pro	Gln	Arg	Lys	Glu	Phe	Asn	Phe	Pro	Glu	Ala	Gly	Ser
									1345					1350
Ser	Ser	Gly	Ala	Leu	Phe	Pro	Ser	Ala	Val	Ser	Pro	Pro	Glu	Leu
									1360					1365
Arg	Gln	Arg	Leu	His	Gly	Val	Glu	Leu	Leu	Lys	Ile	Phe	Asn	Lys
									1375					1380
Asn	Gln	Lys	Leu	Gly	Ser	Ser	Ser	Thr	Ser	Ile	Pro	His	Leu	Ser
									1390					1395
Ser	Pro	Pro	Thr	Lys	Phe	Phe	Val	Ser	Thr	Pro	Ser	Gln	Pro	Ser
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Cys	Lys	Ser	His	Leu	Glu	Thr	Gly	Thr	Lys	Asp	Gln	Glu	Thr	Val
									1420					1425
Cys	Ser	Lys	Ala	Thr	Glu	Gly	Asp	Asn	Thr	Glu	Phe	Gly	Ala	Phe
									1435					1440
Val	Gly	His	Arg	Asp	Ser	Met	Asp	Leu	Gln	Arg	Phe	Lys	Glu	Thr
									1450					1455
Ser	Asn	Lys	Ile	Lys	Ile	Leu	Ser	Asn	Asn	Asn	Thr	Ser	Glu	Asn
									1465					1470
Thr	Leu	Lys	Arg	Val	Ser	Ser	Leu	Ala	Gly	Phe	Thr	Asp	Cys	His
									1480					1485
Arg	Thr	Ser	Ile	Pro	Val	His	Ser	Lys	Gln	Glu	Lys	Ile	Ser	Arg

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Arg Pro Ser Thr Glu Asp Thr His Glu Val	Asp Ser Lys Ala Ala	
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Leu Ile Pro Asp Trp Leu Gln Asp Arg Pro Ser Asn Arg Glu Met		
1520	1525	1530
Pro Ser Glu Glu Gly Thr Leu Asn Gly Leu Thr Ser Pro Phe Lys		
1535	1540	1545
Pro Ala Met Asp Thr Asn Tyr Tyr Tyr Ser Ala Val Glu Arg Asn		
1550	1555	1560
Asn Leu Met Arg Leu Ser Gln Ser Ile Pro Phe Thr Pro Val Pro		
1565	1570	1575
Pro Arg Gly Glu Pro Val Thr Val Tyr Arg Leu Glu Glu Ser Ser		
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Pro Asn Ile Leu Asn Asn Ser Met Ser Ser Trp Ser Gln Leu Gly		
1595	1600	1605
Leu Cys Ala Lys Ile Glu Phe Leu Ser Lys Glu Glu Met Gly Gly		
1610	1615	1620
Gly Leu Arg Arg Ala Val Lys Val Gln Cys Thr Trp Ser Glu His		
1625	1630	1635
Asp Ile Leu Lys Ser Gly His Leu Tyr Ile Ile Lys Ser Phe Leu		
1640	1645	1650
Pro Glu Val Val Asn Thr Trp Ser Ser Ile Tyr Lys Glu Asp Thr		
1655	1660	1665
Val Leu His Leu Cys Leu Arg Glu Ile Gln Gln Gln Arg Ala Ala		
1670	1675	1680
Gln Lys Leu Thr Phe Ala Phe Asn Gln Met Lys Pro Lys Ser Ile		
1685	1690	1695
Pro Tyr Ser Pro Arg Phe Leu Glu Val Phe Leu Leu Tyr Cys His		
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Ser Ala Gly Gln Trp Phe Ala Val Glu Glu Cys Met Thr Gly Glu		
1715	1720	1725
Phe Arg Lys Tyr Asn Asn Asn Asn Gly Asp Glu Ile Ile Pro Thr		
1730	1735	1740
Asn Thr Leu Glu Glu Ile Met Leu Ala Phe Ser His Trp Thr Tyr		
1745	1750	1755
Glu Tyr Thr Arg Gly Glu Leu Leu Val Leu Asp Leu Gln Gly Val		
1760	1765	1770
Gly Glu Asn Leu Thr Asp Pro Ser Val Ile Lys Ala Glu Glu Lys		
1775	1780	1785
Arg Ser Cys Asp Met Val Phe Gly Pro Ala Asn Leu Gly Glu Asp		
1790	1795	1800
Ala Ile Lys Asn Phe Arg Ala Lys His His Cys Asn Ser Cys Cys		
1805	1810	1815
Arg Lys Leu Lys Leu Pro Asp Leu Lys Arg Asn Asp Tyr Thr Pro		
1820	1825	1830
Asp Lys Ile Ile Phe Pro Gln Asp Glu Pro Ser Asp Leu Asn Leu		
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Gln Pro Gly Asn Ser Thr Lys Glu Ser Glu Ser Thr Asn Ser Val		
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Arg Leu Met Leu		

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His Gly Leu Ser Pro	Leu Leu Pro Ala	Arg Gly Gly Gly Ser	Val
35	40	45	
Gly Ser Asp Val Gly	Gln Arg Leu Pro	Val Glu Asp Phe Ser	Leu
50	55	60	
Asp Ser Ser Leu Ser	Gln Val Gln Val	Glu Phe Tyr Val Asn	Glu
65	70	75	
Asn Thr Phe Lys Glu	Arg Leu Lys Leu	Phe Phe Ile Lys Asn	Gln
80	85	90	
Arg Ser Ser Leu Arg	Ile Arg Leu Phe	Asn Phe Ser Leu Lys	Leu
95	100	105	
Leu Thr Cys Leu Leu	Tyr Ile Val Arg	Val Leu Leu Asp Asp	Pro
110	115	120	
Ala Leu Gly Ile Gly	Trp Trp Gly Cys	Pro Arg Gln Asn Tyr	Ser
125	130	135	
Phe Asn Asp Ser Ser	Ser Ser Glu Ile Asn	Trp Ala Pro Ile Leu	Trp
140	145	150	
Val Glu Arg Lys Met	Thr Leu Trp Ala	Ile Gln Val Ile Val	Ala
155	160	165	
Ile Ile Ser Phe Leu	Glu Thr Met Leu	Leu Ile Tyr Leu Ser	Tyr
170	175	180	
Lys Gly Asn Ile Trp	Glu Gln Ile Phe	Arg Val Ser Phe Val	Leu
185	190	195	
Glu Met Ile Asn Thr	Leu Pro Phe Ile	Ile Thr Ile Phe Trp	Pro
200	205	210	
Pro Leu Arg Asn Leu	Phe Ile Pro Val	Phe Leu Asn Cys Trp	Leu
215	220	225	
Ala Lys His Ala Leu	Glu Asn Met Ile	Asn Asp Phe His Arg	Ala
230	235	240	
Ile Leu Arg Thr Gln	Ser Ala Met Phe	Asn Gln Val Leu Ile	Leu
245	250	255	
Phe Cys Thr Leu Leu	Cys Leu Val Phe	Thr Gly Thr Cys Gly	Ile
260	265	270	
Gln His Leu Glu Arg	Ala Gly Glu Asn	Leu Ser Leu Leu Thr	Ser
275	280	285	
Phe Tyr Phe Cys Ile	Val Thr Phe Ser	Thr Val Gly Tyr Gly	Asp
290	295	300	
Val Thr Pro Lys Ile	Trp Pro Ser Gln	Leu Leu Val Val Ile	Met
305	310	315	
Ile Cys Val Ala Leu	Val Val Leu Pro	Leu Gln Phe Glu Glu	Leu
320	325	330	
Val Tyr Leu Trp Met	Glu Arg Gln Lys	Ser Gly Gly Asn Tyr	Ser
335	340	345	
Arg His Arg Ala Gln	Thr Glu Lys His	Val Val Leu Cys Val	Ser
350	355	360	
Ser Leu Lys Ile Asp	Leu Leu Met Asp	Phe Leu Asn Glu Phe	Tyr
365	370	375	
Ala His Pro Arg Leu	Gln Asp Tyr Tyr	Val Val Ile Leu Cys	Pro
380	385	390	
Thr Glu Met Asp Val	Gln Val Arg Arg	Val Leu Gln Ile Pro	Leu
395	400	405	
Trp Ser Gln Arg Val	Ile Tyr Leu Gln	Gly Ser Ala Leu Lys	Asp
410	415	420	
Gln Asp Leu Met Arg	Ala Lys Met Asp	Asn Gly Glu Ala Cys	Phe
425	430	435	
Ile Leu Ser Ser Arg	Asn Glu Val Asp	Arg Thr Ala Ala Asp	His
440	445	450	
Gln Thr Ile Leu Arg	Ala Trp Ala Val	Lys Asp Phe Ala Pro	Asn
455	460	465	
Cys Pro Leu Tyr Val	Gln Ile Leu Lys	Pro Glu Asn Lys Phe	His
470	475	480	

Val	Lys	Phe	Ala	Asp	His	Val	Val	Cys	Glu	Glu	Glu	Cys	Lys	Tyr
				485					490					495
Ala	Met	Leu	Ala	Leu	Asn	Cys	Ile	Cys	Pro	Ala	Thr	Ser	Thr	Leu
				500					505					510
Ile	Thr	Leu	Leu	Val	His	Thr	Ser	Arg	Gly	Gln	Glu	Gly	Gln	Glu
				515					520					525
Ser	Pro	Glu	Gln	Trp	Gln	Arg	Met	Tyr	Gly	Arg	Cys	Ser	Gly	Asn
				530					535					540
Glu	Val	Tyr	His	Ile	Arg	Met	Gly	Asp	Ser	Lys	Phe	Phe	Arg	Glu
				545					550					555
Tyr	Glu	Gly	Lys	Ser	Phe	Thr	Tyr	Ala	Ala	Phe	His	Ala	His	Lys
				560					565					570
Lys	Tyr	Gly	Val	Cys	Leu	Ile	Gly	Leu	Lys	Arg	Glu	Asp	Asn	Lys
				575					580					585
Ser	Ile	Leu	Leu	Asn	Pro	Gly	Pro	Arg	His	Ile	Leu	Ala	Ala	Ser
				590					595					600
Asp	Thr	Cys	Phe	Tyr	Ile	Asn	Ile	Thr	Lys	Glu	Glu	Asn	Ser	Ala
				605					610					615
Phe	Ile	Phe	Lys	Gln	Glu	Glu	Lys	Arg	Lys	Lys	Arg	Ala	Phe	Ser
				620					625					630
Gly	Gln	Gly	Leu	His	Glu	Gly	Pro	Ala	Arg	Leu	Pro	Val	His	Ser
				635					640					645
Ile	Ile	Ala	Ser	Met	Gly	Thr	Val	Ala	Met	Asp	Leu	Gln	Gly	Thr
				650					655					660
Glu	His	Arg	Pro	Thr	Gln	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Lys
				665					670					675
Leu	Ala	Leu	Pro	Thr	Glu	Asn	Gly	Ser	Gly	Ser	Arg	Arg	Pro	Ser
				680					685					690
Ile	Ala	Pro	Val	Leu	Glu	Leu	Ala	Asp	Ser	Ser	Ala	Leu	Leu	Pro
				695					700					705
Cys	Asp	Leu	Leu	Ser	Asp	Gln	Ser	Glu	Asp	Glu	Val	Thr	Pro	Ser
				710					715					720
Asp	Asp	Glu	Gly	Leu	Ser	Val	Val	Glu	Tyr	Val	Lys	Gly	Tyr	Pro
				725					730					735
Pro	Asn	Ser	Pro	Tyr	Ile	Gly	Ser	Ser	Pro	Thr	Leu	Cys	His	Leu
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Leu	Pro	Val	Lys	Ala	Pro	Phe	Cys	Cys	Leu	Arg	Leu	Asp	Lys	Gly
				755					760					765
Cys	Lys	His	Asn	Ser	Tyr	Glu	Asp	Ala	Lys	Ala	Tyr	Gly	Phe	Lys
				770					775					780
Asn	Lys	Leu	Ile	Ile	Val	Ser	Ala	Glu	Thr	Ala	Gly	Asn	Gly	Leu
				785					790					795
Tyr	Asn	Phe	Ile	Val	Pro	Leu	Arg	Ala	Tyr	Tyr	Arg	Ser	Arg	Lys
				800					805					810
Glu	Leu	Asn	Pro	Ile	Val	Leu	Leu	Leu	Asp	Asn	Lys	Pro	Asp	His
				815					820					825
His	Phe	Leu	Glu	Ala	Ile	Cys	Cys	Phe	Pro	Met	Val	Tyr	Tyr	Met
				830					835					840
Glu	Gly	Ser	Val	Asp	Asn	Leu	Asp	Ser	Leu	Leu	Gln	Cys	Gly	Ile
				845					850					855
Ile	Tyr	Ala	Asp	Asn	Leu	Val	Val	Val	Asp	Lys	Glu	Ser	Thr	Met
				860					865					870
Ser	Ala	Glu	Glu	Asp	Tyr	Met	Ala	Asp	Ala	Lys	Thr	Ile	Val	Asn
				875					880					885
Val	Gln	Thr	Met	Phe	Arg	Leu	Phe	Pro	Ser	Leu	Ser	Ile	Thr	Thr
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Glu	Leu	Thr	His	Pro	Ser	Asn	Met	Arg	Phe	Met	Gln	Phe	Arg	Ala
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Lys	Asp	Ser	Tyr	Ser	Leu	Ala	Leu	Ser	Lys	Leu	Glu	Lys	Arg	Glu
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Arg	Glu	Asn	Gly	Ser	Asn	Leu	Ala	Phe	Met	Phe	Arg	Leu	Pro	Phe
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Ala	Ala	Gly	Arg	Val	Phe	Ser	Ile	Ser	Met	Leu	Asp	Thr	Leu	Leu

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 Tyr Gln Ser Phe Val Lys Asp Tyr Met Ile Thr Ile Thr Arg Leu
 965 970 975
 Leu Leu Gly Leu Asp Thr Thr Pro Gly Ser Gly Tyr Leu Cys Ala
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 Met Lys Ile Thr Glu Gly Asp Leu Trp Ile Arg Thr Tyr Gly Arg
 995 1000 1005
 Leu Phe Gln Lys Leu Cys Ser Ser Ser Ala Glu Ile Pro Ile Gly
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 Ile Tyr Arg Thr Glu Ser His Val Phe Ser Thr Ser Glu Pro His
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 Glu Leu Arg Ala Gln Ser Gln Ile Ser Val Asn Val Glu Asp Cys
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 Glu Asp Thr Arg Glu Val Lys Gly Pro Trp Gly Ser Arg Ala Gly
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 Pro Pro Pro Asp Thr Arg Leu Glu Pro Ser Asp Ile Val Tyr Leu
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 Ile Arg Ser Asp Pro Leu Ala His Val Ala Ser Ser Ser Gln Ser
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 35 40 45
 Ala Ile Tyr Trp Cys Thr Glu Val Ile Pro Leu Ala Val Thr Ser
 50 55 60
 Leu Met Pro Val Leu Leu Phe Pro Leu Phe Gln Ile Leu Asp Ser
 65 70 75
 Arg Gln Val Cys Val Gln Tyr Met Lys Asp Thr Asn Met Leu Phe
 80 85 90
 Leu Gly Gly Leu Ile Val Ala Val Ala Val Glu Arg Trp Asn Leu

	95		100		105
His Lys Arg Ile	Ala Leu Arg Thr Leu	Leu Trp Val Gly Ala	Lys		
	110		115		120
Pro Ala Arg Leu	Met Leu Gly Phe Met	Gly Val Thr Ala Leu	Leu		
	125		130		135
Ser Met Trp Ile	Ser Asn Thr Ala Thr	Thr Ala Met Met Val	Pro		
	140		145		150
Ile Val Glu Ala	Ile Leu Gln Gln Met	Glu Ala Thr Ser Ala	Ala		
	155		160		165
Thr Glu Ala Gly	Leu Glu Leu Val Asp	Lys Gly Lys Ala Lys	Glu		
	170		175		180
Leu Pro Ala Asn	Ser Ala Val Pro Thr	Thr Gly Ser Gln Val	Ile		
	185		190		195
Phe Glu Gly Pro	Thr Leu Gly Gln Gln	Glu Asp Gln Glu Arg	Lys		
	200		205		210
Arg Leu Cys Lys	Ala Met Thr Leu Cys	Ile Cys Tyr Ala Ala	Ser		
	215		220		225
Ile Gly Gly Thr	Ala Thr Leu Thr Gly	Thr Gly Pro Asn Val	Val		
	230		235		240
Leu Leu Gly Gln	Met Asn Glu Leu Phe	Pro Asp Ser Lys Asp	Leu		
	245		250		255
Val Asn Phe Ala	Ser Trp Phe Ala Phe	Ala Phe Pro Asn Met	Leu		
	260		265		270
Val Met Leu Leu	Phe Ala Trp Leu Trp	Leu Gln Phe Val Tyr	Met		
	275		280		285
Arg Phe Asn Phe	Lys Lys Ser Trp Gly	Cys Gly Leu Glu Ser	Lys		
	290		295		300
Lys Asn Glu Lys	Ala Ala Leu Lys Val	Leu Gln Glu Glu Tyr	Arg		
	305		310		315
Lys Leu Gly Pro	Leu Ser Phe Ala Glu	Ile Asn Val Leu Ile	Cys		
	320		325		330
Phe Phe Leu Leu	Val Ile Leu Trp Phe	Ser Arg Asp Pro Gly	Phe		
	335		340		345
Met Pro Gly Trp	Leu Thr Val Ala Trp	Val Glu Glu Arg Lys	Thr		
	350		355		360
Pro Phe Tyr Pro	Pro Pro Leu Leu Asp	Trp Lys Val Thr Gln	Glu		
	365		370		375
Lys Val Pro Trp	Gly Ile Val Leu Leu	Leu Gly Gly Gly Phe	Ala		
	380		385		390
Leu Ala Lys Gly	Ser Glu Ala Ser Gly	Leu Ser Val Trp Met	Gly		
	395		400		405
Lys Gln Met Glu	Pro Leu His Ala Val	Pro Pro Ala Ala Ile	Thr		
	410		415		420
Leu Ile Leu Ser	Leu Leu Val Ala Val	Phe Thr Glu Cys Thr	Ser		
	425		430		435
Asn Val Ala Thr	Thr Leu Phe Leu	Pro Ile Phe Ala Ser	Met		
	440		445		450
Ser Arg Ser Ile	Gly Leu Asn Pro Leu	Tyr Ile Met Leu Pro	Cys		
	455		460		465
Thr Leu Ser Ala	Ser Phe Ala Phe Met	Leu Pro Val Ala Thr	Pro		
	470		475		480
Pro Asn Ala Ile	Val Phe Thr Tyr Gly	His Leu Lys Val Ala	Asp		
	485		490		495
Met Val Lys Thr	Gly Val Ile Met Asn	Ile Ile Gly Val Phe	Cys		
	500		505		510
Val Phe Leu Ala	Val Asn Thr Trp Gly	Arg Ala Ile Phe Asp	Leu		
	515		520		525
Asp His Phe Pro	Asp Trp Ala Asn Val	Thr His Ile Glu Thr			
	530		535		

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 <212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7474129CD1

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Met	Lys	Ala	His	Pro	Lys	Glu	Met	Val	Pro	Leu	Met	Gly	Lys	Arg	1	5	10	15
Val	Ala	Ala	Pro	Ser	Gly	Asn	Pro	Ala	Val	Leu	Pro	Glu	Lys	Arg	20	25	30	35
Pro	Ala	Glu	Ile	Thr	Pro	Thr	Lys	Lys	Ser	Ile	Ser	Gly	Asn	Cys	40	45	50	55
Asp	Asp	Met	Asp	Ser	Pro	Gln	Ser	Pro	Gln	Asp	Asp	Val	Thr	Glu	60	65	70	75
Thr	Pro	Ser	Asn	Pro	Asn	Ser	Pro	Ser	Ala	Gln	Leu	Ala	Lys	Glu	80	85	90	95
Glu	Gln	Arg	Arg	Lys	Lys	Arg	Arg	Leu	Lys	Lys	Arg	Ile	Phe	Ala	100	105	110	115
Ala	Val	Ser	Glu	Gly	Cys	Val	Glu	Glu	Leu	Val	Glu	Leu	Leu	Val	120	125	130	135
Glu	Leu	Gln	Glu	Leu	Cys	Arg	Arg	Arg	His	Asp	Glu	Asp	Val	Pro	140	145	150	155
Asp	Phe	Leu	Met	His	Lys	Leu	Thr	Ala	Ser	Asp	Thr	Gly	Lys	Thr	160	165	170	175
Cys	Leu	Met	Lys	Ala	Leu	Leu	Asn	Ile	Asn	Pro	Asn	Thr	Lys	Glu	180	185	190	195
Ile	Val	Arg	Ile	Leu	Leu	Ala	Phe	Ala	Glu	Glu	Asn	Asp	Ile	Leu	200	205	210	215
Gly	Arg	Phe	Ile	Asn	Ala	Glu	Tyr	Thr	Glu	Glu	Ala	Tyr	Glu	Gly	220	225	230	235
Gln	Thr	Ala	Leu	Asn	Ile	Ala	Ile	Glu	Arg	Arg	Gln	Gly	Asp	Ile	240	245	250	255
Ala	Ala	Leu	Leu	Ile	Ala	Ala	Gly	Ala	Asp	Val	Asn	Ala	His	Ala	260	265	270	275
Lys	Gly	Ala	Phe	Phe	Asn	Pro	Lys	Tyr	Gln	His	Glu	Gly	Phe	Tyr	280	285	290	295
Phe	Gly	Glu	Thr	Pro	Leu	Ala	Leu	Ala	Ala	Cys	Thr	Asn	Gln	Pro	300	305	310	315
Glu	Ile	Val	Gln	Leu	Leu	Met	Glu	His	Glu	Gln	Thr	Asp	Ile	Thr	320	325	330	335
Ser	Arg	Asp	Ser	Arg	Gly	Asn	Asn	Ile	Leu	His	Ala	Leu	Val	Thr	340	345	350	355
Val	Ala	Glu	Asp	Phe	Lys	Thr	Gln	Asn	Asp	Val	Val	Lys	Arg	Met	360	365	370	375
Tyr	Asp	Met	Ile	Leu	Leu	Arg	Ser	Gly	Asn	Trp	Glu	Leu	Glu	Thr	380	385	390	395
Thr	Arg	Asn	Asn	Asp	Gly	Leu	Thr	Pro	Leu	Gln	Leu	Ala	Ala	Lys	400	405	410	415
Met	Gly	Lys	Ala	Glu	Ile	Leu	Lys	Tyr	Ile	Leu	Ser	Arg	Glu	Ile	420			
Lys	Glu	Lys	Arg	Leu	Arg	Ser	Leu	Ser	Arg	Lys	Phe	Thr	Asp	Trp				
Ala	Tyr	Gly	Pro	Val	Ser	Ser	Ser	Leu	Tyr	Asp	Leu	Thr	Asn	Val				
Asp	Thr	Thr	Thr	Asp	Asn	Ser	Val	Leu	Glu	Ile	Thr	Val	Tyr	Asn				
Thr	Asn	Ile	Asp	Asn	Arg	His	Glu	Met	Leu	Thr	Leu	Glu	Pro	Leu				
His	Thr	Leu	Leu	His	Met	Lys	Trp	Lys	Lys	Phe	Ala	Lys	His	Met				
Phe	Phe	Leu	Ser	Phe	Cys	Phe	Tyr	Phe	Phe	Tyr	Asn	Ile	Thr	Leu				

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Thr Leu Val Ser Tyr Tyr Arg Pro Arg Glu Glu Glu Ala Ile Pro
425 430 435
His Pro Leu Ala Leu Thr His Lys Met Gly Trp Leu Gln Leu Leu
440 445 450
Gly Arg Met Phe Val Leu Ile Trp Ala Met Cys Ile Ser Val Lys
455 460 465
Glu Gly Ile Ala Ile Phe Leu Leu Arg Pro Ser Asp Leu Gln Ser
470 475 480
Ile Leu Ser Asp Ala Trp Phe His Phe Val Phe Phe Ile Gln Ala
485 490 495
Val Leu Val Ile Leu Ser Val Phe Leu Tyr Leu Phe Ala Tyr Lys
500 505 510
Glu Tyr Leu Ala Cys Leu Val Leu Ala Met Ala Leu Gly Trp Ala
515 520 525
Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln Ser Met Gly Met Tyr
530 535 540
Ser Val Met Ile Gln Lys Val Ile Leu His Asp Val Leu Lys Phe
545 550 555
Leu Phe Val Tyr Ile Val Phe Leu Leu Gly Phe Gly Val Ala Leu
560 565 570
Ala Ser Leu Ile Glu Lys Cys Pro Lys Asp Asn Lys Asp Cys Ser
575 580 585
Ser Tyr Gly Ser Phe Ser Asp Ala Val Leu Glu Leu Phe Lys Leu
590 595 600
Thr Ile Gly Leu Gly Asp Leu Asn Ile Gln Gln Asn Ser Lys Tyr
605 610 615
Pro Ile Leu Phe Leu Phe Leu Leu Ile Thr Tyr Val Ile Leu Thr
620 625 630
Phe Val Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr
635 640 645
Val Glu Asn Val Ser Lys Glu Ser Glu Arg Ile Trp Arg Leu Gln
650 655 660
Arg Ala Arg Thr Ile Leu Glu Phe Glu Lys Met Leu Pro Glu Trp
665 670 675
Leu Arg Ser Arg Phe Arg Met Gly Glu Leu Cys Lys Val Ala Glu
680 685 690
Asp Asp Phe Arg Leu Cys Leu Arg Ile Asn Glu Val Lys Trp Thr
695 700 705
Glu Trp Lys Thr His Val Ser Phe Leu Asn Glu Asp Pro Gly Pro
710 715 720
Val Arg Arg Thr Asp Phe Asn Lys Ile Gln Asp Ser Ser Arg Asn
725 730 735
Asn Ser Lys Thr Thr Leu Asn Ala Phe Glu Glu Val Glu Glu Phe
740 745 750
Pro Glu Thr Ser Val
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<213> Homo sapiens

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<223> Incyte ID No: 7481414CD1

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Met Lys Ser His Pro Ala Ile Gln Ala Ala Ile Asp Leu Thr Ala
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Gly Ala Ala Gly Gly Gly Ala Cys Val Leu Thr Gly Gln Pro Phe
20 25 30
Asp Thr Ile Lys Val Lys Met Gln Thr Phe Pro Gln Leu Tyr Lys
35 40 45

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Gly Leu Ala Asp Cys Phe Leu Lys Thr Tyr Asn Gln Val Gly Ile
 50 55 60
 Arg Gly Leu Tyr Arg Gly Thr Ser Pro Ala Leu Leu Ala Tyr Val
 65 70 75
 Thr Gln Gly Ser Val Leu Phe Met Cys Phe Gly Phe Cys Gln Gln
 80 85 90
 Phe Val Arg Lys Val Ala Arg Val Glu Gln Asn Ala Glu Leu Asn
 95 100 105
 Asp Leu Glu Thr Ala Thr Ala Gly Ser Leu Ala Ser Ala Phe Ala
 110 115 120
 Ala Leu Ala Leu Cys Pro Thr Glu Leu Val Lys Cys Arg Leu Gln
 125 130 135
 Thr Met Tyr Glu Met Lys Met Ser Gly Lys Ile Ala Gln Ser Tyr
 140 145 150
 Asn Thr Ile Trp Ser Met Val Lys Ser Ile Phe Met Lys Asp Gly
 155 160 165
 Pro Leu Gly Phe Tyr Arg Gly Leu Ser Thr Thr Leu Ala Gln Glu
 170 175 180
 Ile Pro Gly Tyr Phe Phe Tyr Phe Gly Gly Tyr Glu Ile Ser Arg
 185 190 195
 Ser Phe Phe Ala Ser Gly Gly Ser Lys Asp Glu Leu Gly Pro Val
 200 205 210
 Pro Leu Met Leu Ser Gly Gly Phe Ala Gly Ile Cys Leu Trp Leu
 215 220 225
 Ile Ile Phe Pro Val Asp Cys Ile Lys Ser Arg Ile Gln Val Leu
 230 235 240
 Ser Met Phe Gly Lys Pro Ala Gly Leu Ile Glu Thr Phe Ile Ser
 245 250 255
 Val Val Arg Asn Glu Gly Ile Ser Ala Leu Tyr Ser Gly Leu Lys
 260 265 270
 Ala Thr Leu Ile Arg Ala Ile Pro Ser Asn Ala Ala Leu Phe Leu
 275 280 285
 Val Tyr Glu Tyr Ser Arg Lys Met Met Met Asn Met Val Glu Glu
 290 295 300
 Tyr

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 Glu Ala Gln Pro Leu Gly Pro Ala Pro Thr Gly Ala Ala Pro Pro
 20 25 30
 Pro Gly Pro Gly Pro Ser Asp Ser Pro Glu Ala Ala Val Glu Lys
 35 40 45
 Val Glu Val Glu Leu Ala Gly Pro Ala Thr Ala Glu Pro His Glu
 50 55 60
 Pro Pro Glu Pro Pro Glu Gly Gly Trp Gly Trp Leu Val Met Leu
 65 70 75
 Ala Ala Met Trp Cys Asn Gly Ser Val Phe Gly Ile Gln Asn Ala
 80 85 90
 Cys Gly Val Leu Phe Val Ser Met Leu Glu Thr Phe Gly Ser Lys
 95 100 105
 Asp Asp Asp Lys Met Val Phe Lys Thr Ala Trp Val Gly Ser Leu
 110 115 120

Ser Met Gly Met	Ile Phe Phe Cys Cys	Pro Ile Val Ser Val Phe	125	130	135
Thr Asp Leu Phe	Gly Cys Arg Lys Thr	Ala Val Val Gly Ala Ala	140	145	150
Val Gly Phe Val	Gly Leu Met Ser Ser	Ser Phe Val Ser Ser Ile	155	160	165
Glu Pro Leu Tyr	Leu Thr Tyr Gly Ile	Ile Phe Ala Cys Gly Cys	170	175	180
Ser Phe Ala Tyr	Gln Pro Ser Leu Val	Ile Leu Gly His Tyr Phe	185	190	195
Lys Lys Arg Leu	Gly Leu Val Asn Gly	Ile Val Thr Ala Gly Ser	200	205	210
Ser Val Phe Thr	Ile Leu Leu Pro Leu	Leu Leu Arg Val Leu Ile	215	220	225
Asp Ser Val Gly	Leu Phe Tyr Thr Leu	Arg Val Leu Cys Ile Phe	230	235	240
Met Phe Val Leu	Phe Leu Ala Gly Phe	Thr Tyr Arg Pro Leu Ala	245	250	255
Thr Ser Thr Lys	Asp Lys Glu Ser Gly	Gly Ser Gly Ser Ser Leu	260	265	270
Phe Ser Arg Lys	Lys Phe Ser Pro Pro	Lys Lys Ile Phe Asn Phe	275	280	285
Ala Ile Phe Lys	Val Thr Ala Tyr Ala	Val Trp Ala Val Gly Ile	290	295	300
Pro Leu Ala Leu	Phe Gly Tyr Phe Val	Pro Tyr Val His Leu Met	305	310	315
Lys His Val Asn	Glu Arg Phe Gln Asp	Glu Lys Asn Lys Glu Val	320	325	330
Val Leu Met Cys	Ile Gly Val Thr Ser	Gly Val Gly Arg Leu Leu	335	340	345
Phe Gly Arg Ile	Ala Asp Tyr Val Pro	Gly Val Lys Lys Val Tyr	350	355	360
Leu Gln Val Leu	Ser Phe Phe Phe Ile	Gly Leu Met Ser Met Met	365	370	375
Ile Pro Leu Cys	Ser Ile Phe Gly Ala	Leu Ile Ala Val Cys Leu	380	385	390
Ile Met Gly Leu	Phe Asp Gly Cys Phe	Ile Ser Ile Met Ala Pro	395	400	405
Ile Ala Phe Glu	Leu Val Gly Ala Gln	Asp Val Ser Gln Ala Ile	410	415	420
Gly Phe Leu Leu	Gly Phe Met Ser Ile	Pro Met Thr Val Gly Pro	425	430	435
Pro Ile Ala Gly	Leu Leu Arg Asp Lys	Leu Gly Ser Tyr Asp Val	440	445	450
Ala Phe Tyr Leu	Ala Gly Val Pro Pro	Leu Ile Gly Gly Ala Val	455	460	465
Leu Cys Phe Ile	Pro Trp Ile His Ser	Lys Lys Gln Arg Glu Ile	470	475	480
Ser Lys Thr Thr	Gly Lys Glu Lys Met	Glu Lys Met Leu Glu Asn	485	490	495
Gln Asn Ser Leu	Leu Ser Ser Ser Ser	Gly Met Phe Lys Lys Glu	500	505	510
Ser Asp Ser Ile	Ile		515		

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<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7472541CD1

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Val	Arg	Asp	Gly	Phe	Pro	His	Cys	Pro	Ser	Glu	Thr	Thr	Pro	Leu	
				20					25					30	
Leu	Ser	Pro	Glu	Lys	Gly	Arg	Gln	Ser	Tyr	Asn	Leu	Thr	Gln	Gln	
				35					40					45	
Arg	Val	Val	Phe	Pro	Asn	Asn	Ser	Ile	Phe	His	Gln	Asp	Trp	Glu	
				50					55					60	
Glu	Val	Ser	Arg	Arg	Tyr	Pro	Gly	Asn	Arg	Thr	Cys	Thr	Thr	Lys	
				65					70					75	
Tyr	Thr	Leu	Phe	Thr	Phe	Leu	Pro	Arg	Asn	Leu	Phe	Glu	Gln	Phe	
				80					85					90	
His	Arg	Trp	Ala	Asn	Leu	Tyr	Phe	Leu	Phe	Leu	Val	Ile	Leu	Ser	
				95					100					105	
Trp	Met	Pro	Ser	Met	Glu	Val	Phe	His	Arg	Glu	Ile	Thr	Met	Leu	
				110					115					120	
Pro	Leu	Ala	Ile	Val	Leu	Phe	Val	Ile	Met	Ile	Lys	Asp	Gly	Met	
				125					130					135	
Glu	Asp	Phe	Lys	Arg	His	Arg	Phe	Asp	Lys	Ala	Ile	Asn	Cys	Ser	
				140					145					150	
Asn	Ile	Arg	Ile	Tyr	Glu	Arg	Lys	Glu	Gln	Thr	Tyr	Val	Gln	Lys	
				155					160					165	
Cys	Trp	Lys	Asp	Val	Arg	Val	Gly	Asp	Phe	Ile	Gln	Met	Lys	Cys	
				170					175					180	
Asn	Glu	Ile	Val	Pro	Ala	Asp	Ile	Leu	Leu	Leu	Phe	Ser	Ser	Asp	
				185					190					195	
Pro	Asn	Gly	Ile	Cys	His	Leu	Glu	Thr	Ala	Ser	Leu	Asp	Gly	Glu	
				200					205					210	
Thr	Asn	Leu	Lys	Gln	Arg	Arg	Val	Val	Lys	Gly	Phe	Ser	Gln	Gln	
				215					220					225	
Glu	Val	Gln	Phe	Glu	Pro	Glu	Leu	Phe	His	Asn	Thr	Ile	Val	Cys	
				230					235					240	
Glu	Lys	Pro	Asn	Asn	His	Leu	Asn	Lys	Phe	Lys	Gly	Tyr	Met	Glu	
				245					250					255	
His	Pro	Asp	Gln	Thr	Arg	Thr	Gly	Phe	Gly	Cys	Glu	Ser	Leu	Leu	
				260					265					270	
Leu	Arg	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Glu	Met	Ala	Val	Gly	Ile	
				275					280					285	
Val	Ile	Tyr	Ala	Gly	His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn	Ser	
				290					295					300	
Gly	Pro	Arg	Tyr	Lys	Arg	Ser	Lys	Ile	Glu	Arg	Arg	Met	Asn	Ile	
				305					310					315	
Asp	Ile	Phe	Phe	Cys	Ile	Gly	Ile	Leu	Ile	Leu	Met	Cys	Leu	Ile	
				320					325					330	
Gly	Ala	Val	Gly	His	Ser	Ile	Trp	Asn	Gly	Thr	Phe	Glu	Glu	His	
				335					340					345	
Pro	Pro	Phe	Asp	Val	Pro	Asp	Ala	Asn	Gly	Ser	Phe	Leu	Pro	Ser	
				350					355					360	
Ala	Leu	Gly	Gly	Phe	Tyr	Met	Phe	Leu	Thr	Met	Ile	Ile	Leu	Leu	
				365					370					375	
Gln	Val	Leu	Ile	Pro	Ile	Ser	Leu	Tyr	Val	Ser	Ile	Glu	Leu	Val	
				380					385					390	
Lys	Leu	Gly	Gln	Val	Phe	Phe	Leu	Ser	Asn	Asp	Leu	Asp	Leu	Tyr	
				395					400					405	
Asp	Glu	Glu	Thr	Asp	Leu	Ser	Ile	Gln	Cys	Arg	Ala	Leu	Asn	Ile	
				410					415					420	
Ala	Glu	Asp	Leu	Gly	Gln	Ile	Gln	Tyr	Ile	Phe	Ser	Asp	Lys	Thr	
				425					430					435	
Gly	Thr	Leu	Thr	Glu	Asn	Lys	Met	Val	Phe	Arg	Arg	Cys	Thr	Ile	
				440					445					450	
Met	Gly	Ser	Glu	Tyr	Ser	His	Gln	Glu	Asn	Ala	Lys	Arg	Leu	Glu	
				455					460					465	

Thr	Pro	Lys	Glu	Leu	Asp	Ser	Asp	Gly	Glu	Glu	Trp	Thr	Gln	Tyr
				470					475					480
Gln	Cys	Leu	Ser	Phe	Ser	Ala	Arg	Trp	Ala	Gln	Asp	Pro	Ala	Thr
				485					490					495
Met	Arg	Ser	Gln	Lys	Gly	Ala	Gln	Pro	Leu	Arg	Arg	Ser	Gln	Ser
				500					505					510
Ala	Arg	Val	Pro	Ile	Gln	Gly	His	Tyr	Arg	Gln	Arg	Ser	Met	Gly
				515					520					525
His	Arg	Glu	Ser	Ser	Gln	Pro	Pro	Val	Ala	Phe	Ser	Ser	Ser	Ile
				530					535					540
Glu	Lys	Asp	Val	Thr	Pro	Asp	Lys	Asn	Leu	Leu	Thr	Lys	Val	Arg
				545					550					555
Asp	Ala	Ala	Leu	Trp	Leu	Glu	Thr	Leu	Ser	Asp	Ser	Arg	Pro	Ala
				560					565					570
Lys	Ala	Ser	Leu	Ser	Thr	Thr	Ser	Ser	Ile	Ala	Asp	Phe	Phe	Leu
				575					580					585
Ala	Leu	Thr	Ile	Cys	Asn	Ser	Val	Met	Val	Ser	Thr	Thr	Thr	Glu
				590					595					600
Pro	Arg	Gln	Arg	Trp	Asp	Asp	Gln	Lys	Ile	Val	Glu	Asn	Asp	His
				605					610					615
Cys	Gln	Cys	Leu	Glu	Phe	Gln	Gly	Trp	Arg	Lys	Ile	Ser	Gly	Phe
				620					625					630
Thr	Tyr	Cys	Lys	Ser	Thr	Phe	Ile	Phe	Arg	Ile	Arg	Gln	Leu	Gly
				635					640					645
Ile	Ile	Ser	Asn	Ile	Glu	Ser	Asn	Ile	Pro	Leu	Ser	Phe	Phe	Gly
				650					655					660
His	Lys	Val	Thr	Ile	Lys	Pro	Ser	Ser	Lys	Ala	Leu	Gly	Thr	Ser
				665					670					675
Leu	Glu	Lys	Ile	Gln	Gln	Leu	Phe	Gln	Lys	Leu	Lys	Leu	Leu	Ser
				680					685					690
Leu	Ser	Gln	Ser	Phe	Ser	Ser	Thr	Ala	Pro	Ser	Asp	Thr	Asp	Leu
				695					700					705
Gly	Glu	Ser	Leu	Gly	Ala	Asn	Val	Ala	Thr	Thr	Asp	Ser	Asp	Glu
				710					715					720
Arg	Asp	Asp	Ala	Ser	Val	Cys	Ser	Gly	Gly	Asp	Ser	Thr	Asp	Asp
				725					730					735
Gly	Gly	Tyr	Arg	Ser	Ser	Met	Trp	Asp	Gln	Gly	Asp	Ile	Leu	Glu
				740					745					750
Ser	Gly	Ser	Gly	Thr	Ser	Leu	Glu	Glu	Ala	Leu	Glu	Ala	Pro	Ala
				755					760					765
Thr	Asp	Leu	Ala	Arg	Pro	Glu	Phe	Cys	Tyr	Glu	Ala	Glu	Ser	Pro
				770					775					780
Asp	Glu	Ala	Ala	Leu	Val	His	Ala	Ala	His	Ala	Tyr	Ser	Phe	Thr
				785					790					795
Leu	Val	Ser	Arg	Thr	Pro	Glu	Gln	Val	Thr	Val	Arg	Leu	Pro	Gln
				800					805					810
Gly	Thr	Cys	Leu	Thr	Phe	Ser	Leu	Leu	Cys	Thr	Leu	Gly	Phe	Asp
				815					820					825
Ser	Val	Arg	Lys	Arg	Met	Ser	Val	Val	Val	Arg	His	Pro	Leu	Thr
				830					835					840
Gly	Glu	Ile	Val	Val	Tyr	Thr	Lys	Gly	Ala	Asp	Ser	Val	Ile	Met
				845					850					855
Asp	Leu	Leu	Glu	Asp	Pro	Ala	Cys	Val	Pro	Asp	Ile	Asn	Met	Glu
				860					865					870
Lys	Lys	Leu	Arg	Lys	Ile	Arg	Ala	Arg	Thr	Gln	Lys	His	Leu	Asp
				875					880					885
Leu	Tyr	Ala	Arg	Asp	Gly	Leu	Arg	Thr	Leu	Cys	Ile	Ala	Lys	Lys
				890					895					900
Val	Val	Ser	Glu	Glu	Asp	Phe	Arg	Arg	Trp	Ala	Ser	Phe	Arg	Arg
				905					910					915
Glu	Ala	Glu	Ala	Ser	Leu	Asp	Asn	Arg	Asp	Glu	Leu	Leu	Met	Glu
				920					925					930
Thr	Ala	Gln	His	Leu	Glu	Asn	Gln	Leu	Thr	Leu	Leu	Gly	Ala	Thr

	935	940	945
Gly Ile Glu Asp Arg Leu Gln Glu Gly	Val Pro Asp Thr Ile Ala		
	950	955	960
Thr Leu Arg Glu Ala Gly Ile Gln Leu	Trp Val Leu Thr Gly Asp		
	965	970	975
Lys Gln Glu Thr Ala Val Asn Ile Ala	His Ser Cys Arg Leu Leu		
	980	985	990
Asn Gln Thr Asp Thr Val Tyr Thr Ile	Asn Thr Glu Asn Gln Glu		
	995	1000	1005
Thr Cys Glu Ser Ile Leu Asn Cys Ala	Leu Glu Glu Leu Lys Gln		
	1010	1015	1020
Phe Arg Glu Leu Gln Lys Pro Asp Arg	Lys Leu Phe Gly Phe Arg		
	1025	1030	1035
Leu Pro Ser Lys Thr Pro Ser Ile Thr	Ser Glu Ala Val Val Pro		
	1040	1045	1050
Glu Ala Gly Leu Val Ile Asp Gly Lys	Thr Leu Asn Ala Ile Phe		
	1055	1060	1065
Gln Gly Lys Leu Glu Lys Lys Phe Leu	Glu Leu Thr Gln Tyr Cys		
	1070	1075	1080
Arg Ser Val Leu Cys Cys Arg Ser Thr	Pro Leu Gln Lys Ser Met		
	1085	1090	1095
Ile Val Lys Leu Val Arg Asp Lys Leu	Arg Val Met Thr Leu Ser		
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Ile Gly Asp Gly Ala Asn Asp Val Ser	Met Ile Gln Ala Ala Asp		
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Ile Gly Ile Gly Ile Ser Gly Gln Glu	Gly Met Gln Ala Val Met		
	1130	1135	1140
Ser Ser Asp Phe Ala Ile Thr Arg Phe	Lys His Leu Lys Lys Leu		
	1145	1150	1155
Leu Leu Val His Gly His Trp Cys Tyr	Ser Arg Leu Ala Arg Met		
	1160	1165	1170
Val Val Tyr Tyr Leu Tyr Lys Asn Val	Cys Tyr Val Asn Leu Leu		
	1175	1180	1185
Phe Trp Tyr Gln Phe Phe Cys Gly Phe	Ser Ser Ser Thr Met Ile		
	1190	1195	1200
Asp Tyr Trp Gln Met Ile Phe Phe Asn	Leu Phe Phe Thr Ser Leu		
	1205	1210	1215
Pro Pro Leu Val Phe Gly Val Leu Asp	Lys Asp Ile Ser Ala Glu		
	1220	1225	1230
Thr Leu Leu Ala Leu Pro Glu Leu Tyr	Lys Ser Gly Gln Asn Ser		
	1235	1240	1245
Glu Cys Tyr Asn Leu Ser Thr Phe Trp	Ile Ser Met Val Asp Ala		
	1250	1255	1260
Phe Tyr Gln Ser Leu Ile Cys Phe Phe	Ile Pro Tyr Leu Ala Tyr		
	1265	1270	1275
Lys Gly Ser Asp Ile Asp Val Phe Thr	Phe Gly Thr Pro Ile Asn		
	1280	1285	1290
Thr Ile Ser Leu Thr Thr Ile Leu Leu	His Gln Ala Met Glu Met		
	1295	1300	1305
Lys Thr Trp Thr Ile Phe His Gly Val	Val Leu Leu Gly Ser Phe		
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Leu Met Tyr Phe Leu Val Ser Leu Leu	Tyr Asn Ala Thr Cys Val		
	1325	1330	1335
Ile Cys Asn Ser Pro Thr Asn Pro Tyr	Trp Val Met Glu Gly Gln		
	1340	1345	1350
Leu Ser Asn Pro Thr Phe Tyr Leu Val	Cys Phe Leu Thr Pro Val		
	1355	1360	1365
Val Ala Leu Leu Pro Arg Tyr Phe Phe	Leu Ser Leu Gln Gly Thr		
	1370	1375	1380
Cys Gly Lys Ser Leu Ile Ser Lys Ala	Gln Lys Ile Asp Lys Leu		
	1385	1390	1395
Pro Pro Asp Lys Arg Asn Leu Glu Ile	Gln Ser Trp Arg Ser Arg		
	1400	1405	1410

Gln Arg Pro Ala Pro Val Pro Glu Val Ala Arg Pro Thr His His
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 Pro Val Ser Ser Ile Thr Gly Gln Asp Phe Ser Ala Ser Thr Pro
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 Lys Ser Ser Asn Pro Pro Lys Arg Lys His Val Glu Glu Ser Val
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 Leu His Glu Gln Arg Cys Gly Thr Glu Cys Met Arg Asp Asp Ser
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 Cys Ser Gly Asp Ser Ser Ala Gln Leu Ser Ser Gly Glu His Leu
 1475 1480 1485
 Leu Gly Pro Asn Arg Ile Met Ala Tyr Ser Gly Gly Gln Thr Asp
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 Ser Leu Thr Ile

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 <213> Homo sapiens

<220>
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 Leu Phe Phe Ser Asn Leu His Gln Val His Asp Thr Pro Gln Met
 50 55 60
 Ser Ser Met Asp Leu Gly Arg Val Asp Ser Phe Asn Asp Thr Asn
 65 70 75
 Tyr Val Ile Ala Phe Ala Pro Glu Ser Lys Thr Thr Gln Glu Ile
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 Met Asn Lys Val Ala Ser Ala Pro Phe Leu Met Ala Gly Arg Thr
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 Ile Met Gly Trp Pro Asp Glu Lys Ser Met Asp Glu Leu Asp Leu
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 Asn Tyr Ser Ile Asp Ala Val Arg Val Ile Phe Thr Asp Thr Phe
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 Ser Tyr His Leu Lys Phe Ser Trp Gly His Arg Ile Pro Met Met
 140 145 150
 Lys Glu His Arg Asp His Ser Ala His Cys Gln Ala Val Asn Glu
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 Lys Met Lys Cys Glu Gly Ser Glu Phe Trp Glu Lys Gly Phe Val
 170 175 180
 Ala Phe Gln Ala Ala Ile Asn Ala Ala Ile Ile Glu Ile Ala Thr
 185 190 195
 Asn His Ser Val Met Glu Gln Leu Met Ser Val Thr Gly Val His
 200 205 210
 Met Lys Ile Leu Pro Phe Val Ala Gln Gly Gly Val Ala Thr Asp
 215 220 225
 Phe Phe Ile Phe Phe Cys Ile Ile Ser Phe Ser Thr Phe Ile Tyr
 230 235 240
 Tyr Val Ser Val Asn Val Thr Gln Glu Arg Gln Tyr Ile Thr Ser
 245 250 255
 Leu Met Thr Met Met Gly Leu Arg Glu Ser Ala Phe Trp Leu Ser
 260 265 270

Trp Gly Leu Met Tyr Ala Gly Phe Ile Leu Ile Met Ala Thr Leu	275	280	285
Met Ala Leu Ile Val Lys Ser Ala Gln Ile Val Val Leu Thr Gly	290	295	300
Phe Val Met Val Phe Thr Leu Phe Leu Leu Tyr Gly Leu Ser Leu	305	310	315
Ile Thr Leu Ala Phe Leu Met Ser Val Leu Ile Lys Lys Pro Phe	320	325	330
Leu Thr Gly Leu Val Val Phe Leu Leu Ile Val Phe Trp Gly Ile	335	340	345
Leu Gly Phe Pro Ala Leu Tyr Thr His Leu Pro Ala Phe Leu Glu	350	355	360
Trp Thr Leu Cys Leu Leu Ser Pro Phe Ala Phe Thr Val Gly Met	365	370	375
Ala Gln Leu Ile His Leu Asp Tyr Asp Val Asn Ser Asn Ala His	380	385	390
Leu Asp Ser Ser Gln Asn Pro Tyr Leu Ile Ile Ala Thr Leu Phe	395	400	405
Met Leu Val Phe Asp Thr Leu Leu Tyr Leu Val Leu Thr Leu Tyr	410	415	420
Phe Asp Lys Ile Leu Pro Ala Glu Tyr Gly His Arg Cys Ser Pro	425	430	435
Leu Phe Phe Leu Lys Ser Cys Phe Trp Phe Gln His Gly Arg Ala	440	445	450
Asn His Val Val Leu Glu Asn Glu Thr Asp Ser Asp Pro Thr Pro	455	460	465
Asn Asp Cys Phe Glu Pro Val Ser Pro Glu Phe Cys Gly Lys Glu	470	475	480
Ala Ile Arg Ile Lys Asn Leu Lys Lys Glu Tyr Ala Gly Lys Cys	485	490	495
Glu Arg Val Glu Ala Leu Lys Gly Val Val Phe Asp Ile Tyr Glu	500	505	510
Gly Gln Ile Thr Ala Leu Leu Gly His Ser Gly Ala Gly Lys Thr	515	520	525
Thr Leu Leu Asn Ile Leu Ser Gly Leu Ser Val Pro Thr Ser Gly	530	535	540
Ser Val Thr Val Tyr Asn His Thr Leu Ser Arg Met Ala Asp Ile	545	550	555
Glu Asn Ile Ser Lys Phe Thr Gly Phe Cys Pro Gln Ser Asn Val	560	565	570
Gln Phe Gly Phe Leu Thr Val Lys Glu Asn Leu Arg Leu Phe Ala	575	580	585
Lys Ile Lys Gly Ile Leu Pro His Glu Val Glu Lys Glu Val Leu	590	595	600
Leu Leu Asp Glu Pro Thr Ala Gly Leu Asp Pro Leu Ser Arg His	605	610	615
Arg Ile Trp Asn Leu Leu Lys Glu Gly Lys Ser Asp Arg Val Ile	620	625	630
Leu Phe Ser Thr Gln Phe Ile Asp Glu Ala Asp Ile Leu Ala Asp	635	640	645
Arg Lys Val Phe Ile Ser Asn Gly Lys Leu Lys Cys Ala Gly Ser	650	655	660
Ser Leu Phe Leu Lys Lys Lys Trp Gly Ile Gly Tyr His Leu Ser	665	670	675
Leu His Leu Asn Glu Arg Cys Asp Pro Glu Ser Ile Thr Ser Leu	680	685	690
Val Lys Gln His Ile Ser Asp Ala Lys Leu Thr Ala Gln Ser Glu	695	700	705
Glu Lys Leu Val Tyr Ile Leu Pro Leu Glu Arg Thr Asn Lys Phe	710	715	720
Pro Glu Leu Tyr Arg Asp Leu Asp Arg Cys Ser Asn Gln Gly Ile	725	730	735
Glu Asp Tyr Gly Val Ser Ile Thr Thr Leu Asn Glu Val Phe Leu			

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Lys Leu Glu Gly	Lys Ser Thr Ile Asp	Glu Ser Asp Ile Gly	Ile		
	755		760		765
Trp Gly Gln Leu	Gln Thr Asp Gly Ala	Lys Asp Ile Gly Ser	Leu		
	770		775		780
Val Glu Leu Glu	Gln Val Leu Ser Ser	Phe His Glu Thr Arg	Lys		
	785		790		795
Thr Ile Ser Gly	Val Ala Leu Trp Arg	Gln Gln Val Cys Ala	Ile		
	800		805		810
Ala Lys Val Arg	Phe Leu Lys Leu Lys	Lys Glu Arg Lys Ser	Leu		
	815		820		825
Trp Thr Ile Leu	Leu Leu Phe Gly Ile	Ser Phe Ile Pro Gln	Leu		
	830		835		840
Leu Glu His Leu	Phe Tyr Glu Ser Tyr	Gln Lys Ser Tyr Pro	Trp		
	845		850		855
Glu Leu Ser Pro	Asn Thr Tyr Phe Leu	Ser Pro Gly Gln Gln	Pro		
	860		865		870
Gln Asp Pro Leu	Thr His Leu Leu Val	Ile Asn Lys Thr Gly	Ser		
	875		880		885
Thr Ile Asp Asn	Phe Leu His Ser Leu	Arg Arg Gln Asn Ile	Ala		
	890		895		900
Ile Glu Val Asp	Ala Phe Gly Thr Arg	Asn Gly Thr Asp Asp	Pro		
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Ser Tyr Asn Gly	Ala Ile Ile Val Ser	Gly Asp Glu Lys Asp	His		
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Arg Phe Ser Ile	Ala Cys Asn Thr Lys	Arg Leu Asn Cys Phe	Pro		
	935		940		945
Val Leu Leu Asp	Val Ile Ser Asn Gly	Leu Leu Gly Ile Phe	Asn		
	950		955		960
Ser Ser Glu His	Ile Gln Thr Asp Arg	Ser Thr Phe Phe Glu	Glu		
	965		970		975
His Met Asp Tyr	Glu Tyr Gly Tyr Arg	Ser Asn Thr Phe Phe	Trp		
	980		985		990
Ile Pro Met Ala	Ala Ser Phe Thr Pro	Tyr Ile Ala Met Ser	Ser		
	995		1000		1005
Ile Gly Asp Tyr	Lys Lys Ala His Ser	Gln Leu Arg Ile	Ser		
	1010		1015		1020
Gly Leu Tyr Pro	Ser Ala Tyr Trp Phe	Gly Gln Ala Leu Val	Asp		
	1025		1030		1035
Val Ser Leu Tyr	Phe Leu Ile Leu Leu	Met Gln Ile Met	Asp		
	1040		1045		1050
Tyr Ile Phe Ser	Pro Glu Glu Ile Ile	Phe Ile Ile Gln Asn	Leu		
	1055		1060		1065
Leu Ile Gln Ile	Leu Cys Ser Ile Gly	Tyr Val Ser Ser Leu	Val		
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Phe Leu Thr Tyr	Val Ile Ser Phe Ile	Phe Arg Asn Gly Arg	Lys		
	1085		1090		1095
Asn Ser Gly Ile	Trp Ser Phe Phe Phe	Leu Ile Val Val Ile	Phe		
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Ser Ile Val Ala	Thr Asp Leu Asn Glu	Tyr Gly Phe Leu Gly	Leu		
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Phe Phe Gly Thr	Met Leu Ile Pro Pro	Phe Thr Leu Ile Gly	Ser		
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Leu Phe Ile Phe	Ser Glu Ile Ser Pro	Asp Ser Met Asp Tyr	Leu		
	1145		1150		1155
Gly Ala Ser Glu	Ser Glu Ile Val Tyr	Leu Ala Leu Leu Ile	Pro		
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Tyr Leu His Phe	Leu Ile Phe Leu Phe	Ile Leu Arg Cys Leu	Glu		
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Met Asn Cys Arg	Lys Lys Leu Met Arg	Lys Asp Pro Val Phe	Arg		
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Ile Ser Pro Arg	Ser Asn Ala Ile Phe	Pro Asn Pro Glu Glu	Pro		
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 Leu Ala Gln Met Glu Pro Leu His Ala Glu Ile Leu Arg Leu Phe
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<210> 37

<211> 3714

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 6996659CB1

<400> 37

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<210> 38

<211> 1009

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472747CB1

<400> 38

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<211> 1155

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7474121CB1

<400> 39

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<210> 40

<211> 2733

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475615CB1

<400> 40

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<210> 41

<211> 3457

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475656CB1

<400> 41

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<211> 5622

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7480632CB1

<400> 42

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<213> Homo sapiens

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<211> 2312

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<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474111CB1

<400> 47

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<211> 2320

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7480826CB1

<400> 48

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<211> 1781

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 6025572CB1

<400> 49

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5686561CB1

<400> 50

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<213> Homo sapiens

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<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7481414CB1

<400> 57

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<213> Homo sapiens

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